GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 15, 2004, 15:11:57 ; Search time 3296.03 Seconds
                                              (without alignments)
                                              10265.033 Million cell updates/sec

Title: US-10-070-532-5
Perfect score: 1133
Sequence: 1 atggagccctcagccacccc..........tcctgaccatcgtgccccgg 1133

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                 1:   em_estba:*
                 2:   em_esthum:*
                 3:   em_estin:*
                 4:   em_estmu:*
                 5:   em_estov:*
                 6:   em_estpl:*
                 7:   em_estro:*
                 8:   em_htc:*
                 9:   gb_est1:*
                 10: gb_est2:*
                 11: gb_htc:*
                 12: gb_est3:*
                 13: gb_est4:*
                 14: gb_est5:*
                 15: em_estfun:*
                 16: em_estom:*
                 17: em_gss_hum:*
                 18: em_gss_inv:*
                 19: em_gss_pln:*
                 20: em_gss_vrt:*
                 21: em_gss_fun:*
                 22: em_gss_mam:*
                 23: em_gss_mus:*
                 24: em_gss_pro:*
                 25: em_gss_rod:*
                 26: em_gss_phg:*
                 27: em_gss_vrl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	715.2	63.1	1740	11	BC035686	BC035686 Homo sapi
c	2	701.4	61.9	886	13	BX433093	BX433093 BX433093
c	3	659.2	58.2	899	13	BX433092	BX433092 BX433092
	4	561.4	49.5	753	29	AY420885	AY420885 Homo sapi
	5	530.4	46.8	3470	11	AK048781	AK048781 Mus muscu
	6	530.4	46.8	3729	11	AK038551	AK038551 Mus muscu
	7	519.8	45.9	1790	11	BC035858	BC035858 Homo sapi
	8	519.4	45.8	3153	11	AK079572	AK079572 Mus muscu
c	9	504.4	44.5	790	14	CF147830	CF147830 AGENCOURT
	10	474.2	41.9	750	29	AY420886	AY420886 Pan trogl
	11	472	41.7	1001	9	AL535838	AL535838 AL535838
	12	468.6	41.4	726	29	AY420887	AY420887 Mus muscu
	13	393.2	34.7	993	12	BM926746	BM926746 AGENCOURT
	14	374.6	33.1	543	13	BX119589	BX119589 BX119589
	15	367	32.4	788	14	CF147829	CF147829 AGENCOURT
	16	329.2	29.1	382	12	BQ042116	BQ042116 sheep1 Sh
c	17	296	26.1	525	12	BI133700	BI133700 UI-M-BH3-
	18	285.4	25.2	635	12	BM939496	BM939496 UI-M-BH3-
	19	278.4	24.6	520	13	BQ269289	BQ269289 ik23f12.y
	20	265.8	23.5	627	10	BB632359	BB632359 BB632359
	21	265.4	23.4	599	12	BM933820	BM933820 UI-M-BH3-
	22	263.2	23.2	611	13	BY723922	BY723922 BY723922
	23	249	22.0	892	13	BX409735	BX409735 BX409735
	24	216.8	19.1	477	12	BM087401	BM087401 500158 MA
	25	202.4	17.9	662	10	BB632883	BB632883 BB632883
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	27	198.2	17.5	1073	12	BM920548	BM920548 AGENCOURT
	28	197.6	17.4	505	10	BB651179	BB651179 BB651179
	29	196.8	17.4	245	12	BI976482	BI976482 485407 MA
	30	186.2	16.4	464	13	BY239887	BY239887 BY239887
	31	175.4	15.5	444	14	R55704	R55704 yg88h10.r1
c	32	165.8	14.6	703	29	CE375359	CE375359 tigr-gss-
	33	163.2	14.4	1290	29	AY411591	AY411591 Homo sapi
	34	162	14.3	721	29	CE235359	CE235359 tigr-gss-
	35	157.8	13.9	1296	29	AY411593	AY411593 Mus muscu
c	36	156.2	13.8	1013	9	AL535837	AL535837 AL535837
	37	147.2	13.0	768	13	BX109847	BX109847 BX109847
	38	133	11.7	257	10	AW427900	AW427900 64510 MAR
c	39	127.2	11.2	1005	28	CC212654	CC212654 CH261-75F
c	40	127.2	11.2	1058	28	CC297061	CC297061 CH261-177
c	41	122.4	10.8	1194	28	CC279941	CC279941 CH261-24C
	42	120.2	10.6	526	29	CG978334	CG978334 CH240_169
	43	119	10.5	1113	29	AY420480	AY420480 Homo sapi
	44	117.8	10.4	1100	29	AY420481	AY420481 Pan trogl
	45	108.8	9.6	1113	29	AY420482	AY420482 Mus muscu

RESULT 1
BC035686

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LOCUS       BC035686              1740 bp    mRNA    linear   HTC 20-SEP-2002
DEFINITION  Homo sapiens, Similar to hypocretin (orexin) receptor 1, clone
            IMAGE:5750551, mRNA.
ACCESSION   BC035686
VERSION     BC035686.1  GI:23242909
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1740)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 79 Row: m Column: 17
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 4557636
            This clone has the following problem: frame shifted.
FEATURES             Location/Qualifiers
     source          1. .1740
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5750551"
                     /tissue_type="Lung, Spleen, fetal, pooled"
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ORIGIN

Query Match   63.1%;   Score 715.2;   DB 11;   Length 1740;
Best Local Similarity 83.3%;   Pred. No. 4.8e-139;
Matches 906; Conservative   0; Mismatches   3; Indels 179; Gaps   1;

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Qy     1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
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Db   506 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 565

Qy    61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db   566 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGCGATTATCTG 625

Qy   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Db   626 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 685

Qy   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
         ||||||||||||||||||
Db   686 CTGGTGGGCAACACGCTG------------------------------------------ 703

Qy   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Db   704 ------------------------------------------------------------ 703

Qy   301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Db   704 ------------------------------------------------------------ 703

Qy   361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
                         ||||||||||||||||||||||||||||||||||||||||||||
Db   704 ----------------GGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 746

Qy   421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db   747 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 806

Qy   481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Db   807 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 866

Qy   541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Db   867 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 926

Qy   601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db   927 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 986

Qy   661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   987 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 1046
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Qy      721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Db     1047 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 1106

Qy      781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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Db     1107 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 1166

Qy      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Db     1167 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1226

Qy      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
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Db     1227 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1286

Qy      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Db     1287 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1346

Qy     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1347 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1406

Qy     1081 CTCAGTGG 1088
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Db     1407 CTCAGTGG 1414
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RESULT 2
BX433093/c
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LOCUS       BX433093                 886 bp    mRNA    linear   EST 15-MAY-2003
DEFINITION  BX433093 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
            CS0DF013YE04 3-PRIME, mRNA sequence.
ACCESSION   BX433093
VERSION     BX433093.1  GI:30779168
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 886)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 151.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0BAI011ZB01_CS00962_2&cluster=151.r.
            Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0BAI011ZB01_CS00962_2.
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FEATURES             Location/Qualifiers
     source          1. .886
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                     /db_xref="taxon:9606"
                     /clone="CS0DF013YE04"
                     /tissue_type="FETAL BRAIN"
                     /dev_stage="fetal"
                     /clone_lib="Homo sapiens FETAL BRAIN"
                     /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-strand cDNA was digested with Not I and
                     cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                     vector. Library was not normalized."
     ORIGIN
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Query Match	61.9%;	Score 701.4; DB 13; Length 886;
Best Local Similarity	99.0%;	Pred. No. 2.8e-136;
Matches 705;	Conservative 0;	Mismatches 7; Indels 0; Gaps 0;

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Qy     377 AGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGT 436
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Db     745 AGGCTGTGTCCGTGTCAGTGACAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGT 686

Qy     437 ATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCC 496
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db     685 ATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATNC 626

Qy     497 TGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCA 556
           ||||||||||| ||||||||||||||||||||||||||||| ||||||||||||| ||||||
Db     625 TGGGCATCTGGCCTGTGTCGCTGGCCATCATGGTGCCCAGGGCTGCAGTCATGCAATGCA 566

Qy     557 GCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCT 616
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     565 GCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCT 506

Qy     617 GGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGG 676
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Db     505 GGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGG 446

Qy     677 CCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCC 736
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Db     445 CCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCC 386

Qy     737 AGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGG 796
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Db     385 AGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGG 326

Qy     797 GGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTG 856
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Db     325 GGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCTG 266

Qy     857 AAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGG 916
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Db     265 AAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGG 206

Qy     917 TCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGA 976
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Qy    977 TGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGC 1036
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Db    145 TGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGC 86


Qy   1037 TGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGG 1088
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Db     85 TGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGG 34
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RESULT 3
BX433092/c
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LOCUS        BX433092                899 bp    mRNA    linear   EST 15-MAY-2003
DEFINITION   BX433092 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
             CS0DF013YE04 3-PRIME, mRNA sequence.
ACCESSION    BX433092
VERSION      BX433092.1  GI:30779167
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 899)
  AUTHORS    Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE      Full-length cDNA libraries and normalization
  JOURNAL    Unpublished (2001)
COMMENT      Contact: Genoscope
             Genoscope - Centre National de Sequencage
             BP 191 91006 EVRY cedex - France
             Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
             Library was constructed by Life Technologies, a division of
             Invitrogen. This sequence belongs to sequence cluster 151.r For
             more information about this cluster, see
             http://www.genoscope.cns.fr/
             cgi-bin/cluster.cgi?seq=CS0BAI011ZB01_CS00962_1&cluster=151.r.
             Contact : Feng Liang Email : fliang@lifetech.com URL :
             http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
             Faraday Avenue Genoscope sequence ID : CS0BAI011ZB01_CS00962_1.
FEATURES             Location/Qualifiers
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                     /clone="CS0DF013YE04"
                     /tissue_type="FETAL BRAIN"
                     /dev_stage="fetal"
                     /clone_lib="Homo sapiens FETAL BRAIN"
                     /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-strand cDNA was digested with Not I and
                     cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                     vector. Library was not normalized."
ORIGIN

  Query Match              58.2%;  Score 659.2;  DB 13;  Length 899;
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      Best Local Similarity   94.4%;  Pred. No. 1.9e-127;
      Matches  693;  Conservative   0;  Mismatches   40;  Indels   1;  Gaps   1;


Qy      372 TCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCG 431
            | ||     |||||||      ||||||||||||||||  ||||||||||||||||  | |||
Db      738 TGTAAGNNCTGTGTCGTGTTCAGTGGCAGTGCTACTTCTCAGCTTCATCGCCTGGACCCG 679

Qy      432 CTGGTATGCCATC-TGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCT 490
            ||||||||||||| | ||||||||||||||||| |  |||||||||||||||||||||||||
Db      678 CTGGTATGCCATCATCCCACCCACTATTGTCAAAGAGCACAGCCCGGCGGGCCCGTGCTC 619

Qy      491 CCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGG 550
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Db      618 CCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGG 559

Qy      551 AATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATG 610
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      558 AATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATG 499

Qy      611 AACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCT 670
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      498 AACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCT 439

Qy      671 ACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGG 730
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      438 ACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGG 379

Qy      731 GCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACC 790
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Db      378 GCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACC 319

Qy      791 AGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCC 850
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Db      318 AGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCCCGCGCCTTCC 259

Qy      851 TGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGC 910
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Db      258 TGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGC 199

Qy      911 TGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGT 970
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Db      198 TGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGT 139

Qy      971 TCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCC 1030
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Db      138 TCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCC 79

Qy     1031 ACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGGAT 1090
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Db       78 ACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTCAACTTCCTCAGGTGCAA 19

Qy     1091 GTAAAGAGAAGAGT 1104
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Db       18 ATTCCGGGAGCAGT 5


RESULT 4
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AY420885
LOCUS   AY420885   753 bp   DNA   linear   GSS 17-DEC-2003
DEFINITION Homo sapiens HCRTR1 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY420885
VERSION   AY420885.1 GI:39776842
KEYWORDS   GSS.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 753)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2 (bases 1 to 753)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT   This sequence as made by sequencing genomic exons and ordering them
            based on alignment.
FEATURES   Location/Qualifiers
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ORIGIN

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Qy   586 ACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTAC 645
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Qy   646 CACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTAT 705
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Db   121 CACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTAT 180

Qy   706 TTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTG 765

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Qy   826 CCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAG 885
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Qy   886 ACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGC 945
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RESULT 5
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LOCUS   AK048781   3470 bp   mRNA   linear   HTC 20-SEP-2003
DEFINITION Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length
            enriched library, clone:C230065B06 product:OREXIN RECEPTOR TYPE 2,
            full insert sequence.
ACCESSION   AK048781
VERSION   AK048781.1 GI:26339571
KEYWORDS   HTC; CAP trapper.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE   High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE   Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,

            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
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            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE   RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE   Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE   Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6 (bases 1 to 3470)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
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            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT   cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.go.jp/
            URL:http://fantom.gsc.riken.go.jp/.
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Qy        80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
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Db       178 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTACACCCGAAAGAATATGAGT 237


Qy       140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
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Db    538  CCATTTGTCACCCTTTGATGTTCAAGAGCACAGCCAAACGGGCTCGAAACAGCATCGTTG  597

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Db    598  TCATCTGGATCGTCTCCTGCATCATAATGATTCCTCAAGCCATTGTCATGGAGTGCAGCA  657

Qy    560  GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGG  619
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Db    718  GCGGTGAAGTTTACCCAAAGATGTACCATATCTGCTTCTTTCTGGTGACATACATGGCAC  777

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Qy    740  TCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGG  799
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Db    838  TTCCCGGAACTTCTTCTGTGGTTCAGAGAAAATGGAAGCAGC------AGCAGCCGGTTT  891

Qy    800  ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAG  859
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RESULT 6
AK038551

LOCUS   AK038551   3729 bp   mRNA   linear   HTC 19-SEP-2003
DEFINITION Mus musculus adult male hypothalamus cDNA, RIKEN full-length
            enriched library, clone:A230036M08 product:OREXIN RECEPTOR TYPE 2,
            full insert sequence.
ACCESSION   AK038551
VERSION   AK038551.1 GI:26332642
KEYWORDS   HTC; CAP trapper.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE   High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE   Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
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            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE   RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE   Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE   Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6   (bases 1 to 3729)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
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            Muramatsu,M. and Hayashizaki,Y.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

COMMENT   cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
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                          /note="unnamed protein product; OREXIN RECEPTOR TYPE 2
                          (SWISSPROT|P56719, evidence: FASTY, 98.5%ID, 100%length,
                          match=1380)
                          putative"
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                          YPKMYHICFFLVTYMAPLCLMILAYLQIFRKLWCRQIPGTSSVVQRKWKQQQPVSQPR
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                          /note="putative"
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  Query Match   46.8%;   Score 530.4;   DB 11;   Length 3729;
  Best Local Similarity   71.1%;   Pred. No. 3.4e-100;
  Matches 718; Conservative   0; Mismatches 286; Indels   6; Gaps   1;

Qy   80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
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Db   179 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTACACCCGAAAGAATATGAGT 238

Qy   140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
            ||||||| ||||||| ||| | |||||||| ||||| || | || ||| ||||

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Db    239  GGGTCCTGATCGCAGGGTATATCATCGTGTTCGTTGTGGCTCTCATCGGGAACGTCCTGG  298

Qy    200  TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA  259
           ||||  ||||  ||||||  ||||||||||||||||||||||||||||||||||||  ||||
Db    299  TCTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACAGTCACCAACTACTTCATAGTCA  358

Qy    260  ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG  319
           ||||  |||||| || || || || ||||||     | ||||||| || || | |||  | || |
Db    359  ACCTTTCCCTAGCAGATGTGCTTGTGACCATCACCTGCCTTCCAGCTACCCTCGTTGTTG  418

Qy    320  ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG  379
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Db    419  ACATCACTGAGACTTGGTTCTTTGGACAGTCCCTCTGTAAGGTCATTCCTTATTTACAGA  478

Qy    380  CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATG  439
           ||||||| ||||| ||| | || || || | |||| ||| ||| ||||||| |||||| |
Db    479  CTGTGTCAGTGTCTGTGTCTGTTCTTACGTTGAGCTGCATTGCCTTGGACCGATGGTACG  538

Qy    440  CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG  499
           |||| || |||||  | ||||||||||||||||||  |||||| ||  | |||| | |
Db    539  CCATTTGTCACCCTTTGATGTTCAAGAGCACAGCCAAACGGGCTCGAAACAGCATCGTTG  598

Qy    500  GCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCA  559
           ||||||| || || ||| ||| || || || || ||||||||| |||||||
Db    599  TCATCTGGATCGTCTCCTGCATCATAATGATTCCTCAAGCCATTGTCATGGAGTGCAGCA  658

Qy    560  GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGG  619
           | |||| |||| |||||||| || ||||| |||| ||||||||||||| |||||
Db    659  GCATGCTCCCTGGCCTAGCCAATAAGACCACCCTCTTTACAGTATGTGATGAACACTGGG  718

Qy    620  CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCC  679
           | |||  | || || ||||| ||||| | |||||||||| | || || ||| |||| |
Db    719  GCGGTGAAGTTTACCCAAAGATGTACCATATCTGCTTCTTTCTGGTGACATACATGGCAC  778

Qy    680  CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA  739
           | ||| | || ||| |||| ||| || |||| ||||||||| || |||||| |||| ||||
Db    779  CTCTGTGTCTTATGATATTGGCTTATCTCCAAATATTCCGTAAACTCTGGTGCCGACAGA  838

Qy    740  TCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGG  799
           | |||||| ||  | || |   |  | | || |||||||| |        | |||| ||
Db    839  TTCCCGGAACTTCTTCTGTGGTTCAGAGAAAATGGAAGCAGC------AGCAGCCGGTTT  892

Qy    800  ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAG  859
           | |    | |||      |   || | || | || | |||     |||| |      |||||
Db    893  CTCAGCCCCGGGGGTCCGGACAGCAGAGCAAGGCTCGGATTAGCGCTGTTGCTGCTGAGA  952

Qy    860  TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCT  919
           | |||||||| ||| |||| |  ||||| || ||||| |||| ||||| || || |||||||
Db    953  TAAAGCAGATCCGAGCACGAAGGAAAACAGCCCGGATGCTCATGGTTGTACTTCTGGTCT  1012

Qy    920  TCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGT  979
           | ||  | ||||| || || |||||||| ||||||||  || ||||| || || |||||||
Db    1013 TTGCAATTTGCTATCTACCAATCAGCATCCTCAATGTGCTAAAGAGAGTATTTGGGATGT  1072

Qy    980  TCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGG  1039
           ||  |  || |   ||| | || |||||||| || || ||||| || || ||  ||||||| |
Db    1073 TCACACACACGGAAGACAGAGAGACTGTCTATGCTTGGTTCACTTTTTTCTCATTGGCTTG  1132
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·Qy      1040 TGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGGA 1089
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RESULT 7
BC035858
LOCUS   BC035858   1790 bp   mRNA   linear   HTC 04-MAR-2003
DEFINITION Homo sapiens, Similar to hypocretin (orexin) receptor 2, clone
            IMAGE:5767576, mRNA.
ACCESSION   BC035858
VERSION   BC035858.1 GI:23959160
KEYWORDS   HTC.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1790)
  AUTHORS   Strausberg,R.
  TITLE   Direct Submission
  JOURNAL   Submitted (31-JUL-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 79 Row: p Column: 14
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 6006037
            This clone has the following problem: retained intron.
FEATURES   Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5767576"
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/tissue_type="Brain, fetal, whole pooled"
                    /clone_lib="NIH_MGC_121"
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                    /note="Vector: pCMV-SPORT6"
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          Query Match            45.9%;   Score 519.8;  DB 11;  Length 1790;
          Best Local Similarity  70.5%;   Pred. No. 4e-98;
          Matches  711;  Conservative    0;  Mismatches  292;  Indels    6;  Gaps    1;


        Qy         80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
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        Qy        200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
                      | || |||| |||||| |||||||||||||||||||| || |||||||||||||| ||||
        Db        266 TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA 325

        Qy        260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
                      | || || |||||||| || || |||||| | |||||| || |||| ||| | ||||
        Db        326 ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCCAGCCACACTGGTCGTGG 385

        Qy        320 ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG 379
                      | ||||||||| ||||| | || || || |||| ||||| || || || |||||||||
        Db        386 ATATCACTGAGACCTGGTTTTTTGGACAGTCCCTTTGCAAAGTGATTCCTTATCTACAGA 445

        Qy        380 CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATG 439
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        Db        446 CCGTGTCGGTGTCTGTGTCTGTCCTCACACTGAGCTGTATCGCCTTGGATCGGTGGTATG 505

        Qy        440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG 499
                      | |||||| ||||| | |||| |||||||||||| ||||||||| | ||| |
        Db        506 CAATCTGTCACCCTTTGATGTTTAAGAGCACAGCAAAGCGGGCCCGTAACAGCATTGTCA 565

        Qy        500 GCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCA 559
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        Db        566 TCATCTGGATTGTCTCCTGCATTATAATGATTCCTCAGGCCATCGTCATGGAGTGCAGCA 625

        Qy        560 GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGG 619
                      ||| | || | ||||||| || ||||| | || ||||||||| |||||||
        Db        626 CCGTGTTCCCAGGCTTAGCCAATAAAACCACCCTCTTTACGGTGTGTGATGAGCGCTGGG 685

        Qy        620 CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCC 679
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        Db        686 GTGGTGAAATTTATCCCAAGATGTACCACATCTGTTTCTTTCTGGTGACATACATGGCAC 745

        Qy        680 CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA 739
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        Db        746 CACTGTGTCTCATGGTGTTGGCTTATCTGCAAATATTTCGCAAACTCTGGTGTCGACAGA 805

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Qy     800 ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAG 859
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Qy     860 TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCT 919
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Db    1040 TTGCCCATACTGAAGACAGAGAGACTGTGTATGCCTGGTTTACCTTTTCACACTGGCTTG 1099

Qy    1040 TGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGG 1088
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RESULT 8
AK079572

LOCUS   AK079572   3153 bp   mRNA   linear   HTC 19-SEP-2003
DEFINITION   Mus musculus adult male hypothalamus cDNA, RIKEN full-length
               enriched library, clone:A230091E19 product:OREXIN RECEPTOR TYPE 2,
               full insert sequence.
ACCESSION   AK079572
VERSION   AK079572.1 GI:26348079
KEYWORDS   HTC; CAP trapper.
SOURCE   Mus musculus (house mouse)
  ORGANISM   Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE   High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
               Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE   Normalization and subtraction of cap-trapper-selected cDNAs to
               prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
               Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
               Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
               Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
               Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
               Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
               Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE   RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE   20530913
PUBMED   11076861
REFERENCE   4
AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
TITLE   Functional annotation of a full-length mouse cDNA collection
JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
TITLE   Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6 (bases 1 to 3153)
AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
TITLE   Direct Submission
JOURNAL   Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT   cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.go.jp/
            URL:http://fantom.gsc.riken.go.jp/.
FEATURES   Location/Qualifiers
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                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM_DB:A230091E19"
                     /db_xref="MGI:2403517"
                     /db_xref="taxon:10090"
                     /clone="A230091E19"
                     /sex="male"
                     /tissue_type="hypothalamus"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"

  Query Match   45.8%;   Score 519.4;   DB 11;   Length 3153;
  Best Local Similarity   71.0%;   Pred. No. 6.3e-98;
    Matches 718; Conservative   0; Mismatches 286;   Indels   7; Gaps   2;

Qy   80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
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Qy   140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
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Qy   200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
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Qy   260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
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Qy   320 ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG 379
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Qy   380 CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATG 439
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Db   511 CTGTGTCAGTGTCTGTGTCTGTTCTTACGTTGAGCTGCATTGCCTTGGACCGATGGTACG 570

Qy   440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG 499
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Db   571 CCATTTGTCACCCTTTGATGTTCAAGAGCACAGCCAAACGGGCTCGAAACAGCATCGTTG 630

Qy   500 GCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCA 559
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Db   631 TCATCTGGATCGTCTCCTGCATCATAATGATTCCTCAAGCCATTGTCATGGAGTGCAGCA 690

Qy   560 GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGG 619
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Qy        620 CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCC 679
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Qy        800 ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAG 859
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Db        925 CTCAGCCCCGGGGGTCCGGACAGCAGAGCAAGGCTCGGGTTAGCGCTGTTGCTGCTGAGA 984

Qy        860 TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCT 919
              | |||||||| || ||||| ||||| |||||| |||||| ||||| || || |||||||
Db        985 TAAAGCAGATCCGAGCACGAAGGAAAACAGCCCGGATGCTCATGGTTGTACTTCTGGTCT 1044

Qy        920 TCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGT 979
              | || | ||||| || || ||||| ||||||||| || ||||| || || ||||||||
Db       1045 TTGCAATTTGCTATCTACCAATCAGCATCCTCAATGTGCTAAAGAGAGTATTTGGGATGT 1104

Qy        980 TCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGG 1039
              || || | ||| | || ||||||| || || |||||| || | || ||||| |
Db       1105 TCACACACACGGAAGACAGAGAGACTGTCTATGCTTGGTTCACTTTTCCTCATTGGCTTG 1164

Qy       1040 TGTACGCCAACAGC-GCTGCCAACCCCATCATCTACAACTTCCTCAGTGGA 1089
              | || ||||||||| ||||| ||||| || || || || || || ||||||
Db       1165 TATATGCCAACAGCTGCTGCAAACCCAATTATTTATAATTTTCTTAGTGGA 1215
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RESULT 9
CF147830/c

FEATURES   Location/Qualifiers
     source   1. .790
                         /organism="Homo sapiens"
                         /mol_type="mRNA"
                         /db_xref="taxon:9606"
                         /clone="IMAGE:6971889"
                         /tissue_type="mixed"
                         /lab_host="DH10B"
                         /clone_lib="NIH_MGC_145"
                         /note="Vector: pcDNA3.1; Site_1: varies by clone; Site_2:
                         varies by clone; ORFs were PCR-amplified and cloned into
                         pcDNA3.1 by the GPCR Consortium. Cloning sites vary by
                         clone and include the following: 5'-EcoRV-XmnI/XhoI-3',
                         5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).
                         For information about which gene each clones represents,
                         please visit our anonymous ftp site at
                         ftp://image.llnl.gov/image/rearrayed_plates/IRBI.preSV.dat
                         a Note: this is a NIH_MGC Library."
     ORIGIN

   Query Match   44.5%;   Score 504.4;   DB 14;   Length 790;
   Best Local Similarity   99.8%;   Pred. No. 4.7e-95;
   Matches   505;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

Qy   583 CGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATC 642
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   790 CGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATC 731

Qy   643 TACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCC 702
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   730 TACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCC 671

Qy   703 TATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTG 762
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   670 TATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTG 611

Qy   763 GTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGA 822
            |||||||||||||||||||||||||||||||||||i;ii|||||||||||||||||||||||
Db   610 GTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGA 551

Qy   823 GAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGG 882
            |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db   550 GAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGG 491

Qy   883 AAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATC 942
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   490 AAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATC 431

Qy   943 AGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAA 1002

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                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      430 AGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAA 371


Qy     1003 GCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAAC 1062
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      370 GCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAAC 311


Qy     1063 CCCATCATCTACAACTTCCTCAGTGG 1088
                  ||||||||||||||||||||||||||
Db      310 CCCATCATCTACAACTTCCTCAGTGG 285
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RESULT 10
AY420886
LOCUS   AY420886   750 bp   DNA   linear   GSS 17-DEC-2003
DEFINITION   Pan troglodytes HCRTR1 gene, VIRTUAL TRANSCRIPT, partial sequence,
             genomic survey sequence.
ACCESSION   AY420886
VERSION   AY420886.1 GI:39776843
KEYWORDS   GSS.
SOURCE   Pan troglodytes (chimpanzee)
  ORGANISM   Pan troglodytes
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1 (bases 1 to 750)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
             Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
             Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
             Adams,M.D. and Cargill,M.
  TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
             gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
  PUBMED   14671302
REFERENCE   2 (bases 1 to 750)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
             Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
             Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
             Adams,M.D. and Cargill,M.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
             Rockville, MD 20850, USA
COMMENT   This sequence as made by sequencing genomic exons and ordering them
             based on alignment.
FEATURES   Location/Qualifiers
     source   1. .750
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     gene   <1. .>750
                     /gene="HCRTR1"
                     /locus_tag="HCM7373"
ORIGIN

     Query Match   41.9%;   Score 474.2;   DB 29;   Length 750;
     Best Local Similarity 84.5%;   Pred. No. 9.7e-89;
     Matches 476;   Conservative   0;   Mismatches   87;   Indels   0;   Gaps   0;

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Qy      526 ATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGC 585
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGC 60

Qy      586 ACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTAC 645
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 ACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTAC 120

Qy      646 CACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTAT 705
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 CACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTAT 180

Qy      706 TTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTG 765
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 TTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTG 240

Qy      766 CGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAG 825
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 CGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAG 300

Qy      826 CCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAG 885
            ||||||||||||| |||||||||||||||||||||||||||||||||||| |||||||||
Db      301 CCCCAGCCCCGGGCCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCGCGGAGGAAG 360

Qy      886 ACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGC 945
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 ACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGT 420

Qy      946 GTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCT 1005
            ||||||||||||||||||||||
Db      421 GTCCTCAATGTCCTTAAGAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 480

Qy     1006 GTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCC 1065
                                                     |||||||||    |||||||||
Db      481 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNACGCCAACAGNNNGCCAACCCC 540

Qy     1066 ATCATCTACAACTTCCTCAGTGG 1088
            ||||    |||||||||||||||
Db      541 ATCANNNACAACTTCCTCAGTGG 563
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RESULT 11
AL535838

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COMMENT          On Feb 13, 2001 this sequence version replaced gi:12799331.
                 Contact: Genoscope
                 Genoscope - Centre National de Sequencage
                 BP 191 91006 EVRY cedex - France
                 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
                 Library was constructed by Life Technologies, a division of
                 Invitrogen. This sequence belongs to sequence cluster 151.r For
                 more information about this cluster, see
                 http://www.genoscope.cns.fr/
                 cgi-bin/cluster.cgi?seq=CS0DF013BC02QP1&cluster=151.r. Contact :
                 Feng Liang Email : fliang@lifetech.com URL :
                 http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                 Faraday Avenue Genoscope sequence ID : CS0DF013BC02QP1.
FEATURES                 Location/Qualifiers
     source              1. .1001
                         /organism="Homo sapiens"
                         /mol_type="mRNA"
                         /db_xref="taxon:9606"
                         /clone="CS0DF013YE04"
                         /tissue_type="FETAL BRAIN"
                         /dev_stage="fetal"
                         /clone_lib="Homo sapiens FETAL BRAIN"
                         /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
                         was primed with a NotI-oligo(dT) primer. Five prime end
                         enriched, double-strand cDNA was digested with Not I and
                         cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                         vector. Library was not normalized."
ORIGIN

  Query Match               41.7%;  Score 472;  DB 9;  Length 1001;
  Best Local Similarity     92.0%;  Pred. No. 3.2e-88;
  Matches  544;  Conservative  13;  Mismatches  25;  Indels  9;  Gaps  6;


Qy     377 AGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGT 436
           |||||||||||||||| |||||||||||||||||:| ||||||||:|||||||||||||||
Db     415 AGGCTGTGTCCGTGTCANTGGCAGTGCTAACTCTMANCTTCATCGCMCTGGACCGCTGGT 474


Qy     437 ATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCC 496
           ||||:|||||:||||||||||||||||||||||:||||||||||||||||||||||||||
Db     475 ATGCHATCTGCYACCCACTATTGTTCAAGARCACAGCCCGGCGGGCCCGTGGCTCCATCC 534


Qy     497 TGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCA 556
           |  |  ||||||||| | |||||||||||||||||||||||||||||||||||||||||||
Db     535 TNNGNATCTGGGCTNTNTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCA 594


Qy     557 GCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCT 616
           |||||||||||||| ||||| ||||||||||||||||||||||||||||||||||||||||
Db     595 GCAGTGTGCTGCCTNAGCTANCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCT 654


Qy     617 GGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGG 676
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     655 GGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGG 714


Qy     677 CCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCC 736
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     715 CCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCC 774
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Qy    737 AGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCT-G 795
          |·|||||||||||||||||||||||||·||||||||||||||||||||||||||||||| |
Db    775 AGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGG 834

Qy    796 GGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCT 855
          |||||||||||||||||||||||||||||||||||||    ||| |||||||||||||||||
Db    835 GGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCC--AGCCCCGGGCCGCGCCTTCCTGGCT 892

Qy    856 GAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTG 915
          ||||||| : | |     || |:|||||:|:|||||||||||||||||||:||||||||
Db    893 GAAGTGA---RCAGATGSTGCAGGCAGVAGACASCSAAGATGCTGATGGTGGBGCTGCTG 949

Qy    916 GTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGG 966
          :|||||| |||||||||||:|| |||||||:|| |||||||||| | ||||||
Db    950 STCTTCG-CCTCTGCTACSTG-CCATCAGSGT-CTCAATGTCTTAAAGAGG 997
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RESULT 12
AY420887
LOCUS   AY420887   726 bp   DNA   linear   GSS 17-DEC-2003
DEFINITION   Mus musculus HCRTR1 gene, VIRTUAL TRANSCRIPT, partial sequence,
             genomic survey sequence.
ACCESSION   AY420887
VERSION   AY420887.1 GI:39776844
KEYWORDS   GSS.
SOURCE   Mus musculus (house mouse)
  ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 726)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
             Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
             Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
             Adams,M.D. and Cargill,M.
  TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
             gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
  PUBMED   14671302
REFERENCE   2 (bases 1 to 726)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
             Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
             Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
             Adams,M.D. and Cargill,M.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
             Rockville, MD 20850, USA
COMMENT   This sequence as made by sequencing genomic exons and ordering them
             based on alignment.
FEATURES   Location/Qualifiers
     source   1. .726
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
     gene   <1. .>726
                     /gene="HCRTR1"
                     /locus_tag="HCM7373"
ORIGIN

Query Match   41.4%;   Score 468.6;   DB 29;   Length 726;
Best Local Similarity 89.5%;   Pred. No. 1.4e-87;
Matches 504; Conservative   0; Mismatches   59; Indels   0; Gaps   0;

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Qy    526 ATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGC 585
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Db      1 ATGGTGCCCCAGGCTGCTGTCATGGAGTGCAGCAGCGTGCTGCCTGAGCTAGCCAATCGC 60

Qy    586 ACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTAC 645
          || ||||||||||| |||||||||| | ||||||||||| ||||| ||||||||||||||
Db     61 ACCCGGCTCTTCTCTGTCTGTGATGAGCACTGGGCAGATGAACTCTACCCCAAGATCTAT 120

Qy    646 CACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTAT 705
          ||||| |||||| || ||||||||||||||||||||||||||||||||| ||||||||||
Db    121 CACAGCTGCTTTTTCATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCTATGGCCTAT 180

Qy    706 TTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTG 765
          |||||||| ||||||||||||||||||||||||||||| || ||||| |||||  |||||
Db    181 TTCCAGATCTTCCGCAAGCTCTGGGGCCGCCAGATCCCTGGTACCACATCAGCCTTGGTG 240

Qy    766 CGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAG 825
          |||||||||| || ||||| || || |||| || | | | ||||||||| || ||||
Db    241 CGGAACTGGAAACGGCCCTCGGAACAACTGGAGGCTCAGCACCAGGGCCTCTGTACAGAG 300

Qy    826 CCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAG 885
          |||||||||||||||| ||| |||||||||||| ||||||||||||||| || |||||||||
Db    301 CCCCAGCCCCGGGCCCGAGCCTTCCTGGCTGAGGTGAAGCAGATGCGAGCTCGGAGGAAG 360

Qy    886 ACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGC 945
          || || ||||||||||||||| || ||||||| || || ||||| || |||||||||||
Db    361 ACGGCTAAGATGCTGATGGTAGTCCTGCTGGTTTTTGCACTCTGTTATCTGCCCATCAGT 420

Qy    946 GTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCT 1005
          ||||||||||||||||||||| |||||||||||||||||||||||||| ||||| |||||
Db    421 GTCCTCAATGTCCTTAAGAGAGTGTTCGGGATGTTCCGCCAAGCCAGCGACCGGGAAGCC 480

Qy   1006 GTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCC 1065
          ||||||||||||||||||||||||||||||||| |||||||||||||| || ||||||||
Db    481 GTCTACGCCTGCTTCACCTTCTCCCACTGGCTAGTGTACGCCAACAGTGCCGCCAACCCT 540

Qy   1066 ATCATCTACAACTTCCTCAGTGG 1088
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Db    541 ATCATCTACAACTTCCTCAGTGG 563
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RESULT 13
BM926746
LOCUS   BM926746   993 bp   mRNA   linear   EST 12-MAR-2002
DEFINITION AGENCOURT_6681991 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5767576
            5', mRNA sequence.
ACCESSION   BM926746
VERSION   BM926746.1 GI:19377125
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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                    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1   (bases 1 to 993)
  AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
  TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL    Unpublished (1999)
  COMMENT    Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Life Technologies, Inc.
              cDNA Library Preparation: Life Technologies, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLAM12826  row: a  column: 17
             High quality sequence stop: 684.
FEATURES                Location/Qualifiers
     source             1. .993
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone="IMAGE:5767576"
                        /lab_host="DH10B"
                        /clone_lib="NIH_MGC_121"
                        /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                        Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                        fetal brains, female age 20 weeks, female age 24 weeks,
                        and male age 26 weeks.  Library is oligo-dT primed and
                        directionally cloned (EcoRV site is destroyed  upon
                        cloning).  Average insert size 1.7 kb, insert size range
                        0.7-3.5 kb.  Library is normalized and enriched for
                        full-length clones and  was constructed by C. Gruber
                        (Invitrogen).  Research Genetics  tracking code 017. Note:
                        this is a NIH_MGC Library."
ORIGIN

   Query Match              34.7%;  Score 393.2;  DB 12;  Length 993;
   Best Local Similarity   .72.1%;  Pred. No. 1e-71;
   Matches   512;  Conservative    0;  Mismatches  198;  Indels    0;  Gaps    0;


Qy        80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
             I II II II II II II II II IIIIII I II II III IIII III I IIIIIII
Db       145 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTGCACCCGAAAGAATATGAGT 204


Qy       140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
             IIIIIII II IIIIII I  II   I      IIIIIIIIIIIIIII II I II III IIIII
Db       205 GGGTCCTGATCGCCGGGTACATCATCGTGTTCGTCGTGGCTCTCATTGGGAACGTCCTGG 264


Qy       200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
             I II  IIII IIIIII  IIIIIIIIIIIIIIIIII II IIIIIIIIIIIIIII IIII
Db       265 TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA 324


Qy       260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
             I II II IIIIIIIII II II IIIII    I IIIIII II IIII III I IIII
Db       325 ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCCAGCCACACTGGTCGTGG 384


Qy       320 ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG 379
```

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          | |||||||||| ||||| | || || ||  |||| ||||| || || || ||||||||||
Db    385 ATATCACTGAGACCTGGTTTTTTGGACAGTCCCTTTGCAAAGTGATTCCTTATCTACAGA 444

Qy    380 CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATG 439
          | |||||| ||||| ||| | || || || || |||| |||||| |||| || ||||||||
Db    445 CCGTGTCGGTGTCTGTGTCTGTCCTCACACTGAGCTGTATCGCCTTGGATCGGTGGTATG 504

Qy    440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG 499
          | |||||| ||||| |  |||| |||||||||||  |||||||||| | ||| |
Db   .505 CAATCTGTCACCCTTTGATGTTTAAGAGCACAGCAAAGCGGGCCCGTAACAGCATTGTCA 564

Qy    500 GCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCA 559
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Db    565 TCATCTGGATTGTCTCCTGCATTATAATGATTCCTCAGGCCATCGTCATGGAGTGCAGCA 624

Qy    560 GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGG 619
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Db    625 CCGTGTTCCCAGGCTTAGCCAATAAAACCACCCTCTTTACGGTGTGTGATGAGCGCTGGG 684

Qy    620 CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCC 679
          | |||  | |||||||||||| |||||||  || |||||| | || || ||| |||| |
Db    685 GTGGTGAAATTTATCCCAAGATGTACCACATCTGTTTCTTTCTGGTGACATACATGGCAC 744

Qy    680 CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA 739
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Db    745 CACTGTGTCTCATGGTGTTGGCTTATCTGCAAATATTTCGCAAACTCTGGTGTCGACAGA 804

Qy    740 TCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGAC 789
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Db    805 TCCCTGGAACATCATCTGTAGTTCAGAGAAAATGGAAAGCCCCTGGAGCC 854
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RESULT 14
BX119589
LOCUS   BX119589   543 bp   mRNA   linear   EST 10-FEB-2003
DEFINITION   BX119589 Soares infant brain 1NIB Homo sapiens cDNA clone
             IMAGp998P20171 ; IMAGE:40608, mRNA sequence.
ACCESSION   BX119589
VERSION   BX119589.1 GI:28289997
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 543)
  AUTHORS   Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
             Radelof,U., Schneider,D. and Korn,B.
  TITLE   Human UnigeneSet - RZPD3
  JOURNAL   Unpublished (2003)
COMMENT   Contact: Ina Rolfs
             RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
             Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
             RZPD; IMAGp998P20171.
             RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
             Human UnigeneSet - RZPD3 (RZPDLIB No.972)
             http://www.rzpd.de/CloneCards/cgi-
             bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs

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FEATURES              Location/Qualifiers
     source           1. .543
                      /organism="Homo sapiens"
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                      /db_xref="taxon:9606"
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                      /sex="female"
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                      /clone_lib="Soares infant brain 1NIB"
                      /note="Organ: whole brain; Vector: Lafmid BA; Site_1: Not
                      I; Site_2: Hind III; 1st strand cDNA was primed with a Not
                      I - oligo(dT) primer [5'
                      AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTTT 3'];
                      double-stranded cDNA was ligated to Hind III adaptors
                      (Pharmacia), digested with Not I and directionally cloned
                      into the Not I and Hind III sites of the Lafmid BA vector.
                      Library went through one round of normalization. Library
                      constructed by Bento Soares and M.Fatima Bonaldo."
ORIGIN
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  Query Match                33.1%;  Score 374.6;  DB 13;  Length 543;
  Best Local Similarity      98.7%;  Pred. No. 6e-68;
  Matches  377;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
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Db       158 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 217

Qy        61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db       218 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGCGATTATCTG 277

Qy       121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       278 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 337

Qy       181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db       338 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 397

Qy       241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       398 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 457

Qy       301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db       458 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGNAAG 517
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Qy          361 GTCATCCCCTATCTACAGGCTG 382
                |||||||||||||||||||| | |.
Db          518 GTCATCCCCTATCTACAGACAG 539
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RESULT 15
CF147829
LOCUS   CF147829   788 bp   mRNA   linear   EST 25-JUL-2003
DEFINITION   AGENCOURT_14740210 NIH_MGC_145 Homo sapiens cDNA clone
               IMAGE:6971890 5', mRNA sequence.
ACCESSION   CF147829
VERSION   CF147829.1 GI:33244097
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 788)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Daniela S. Gerhard, Ph.D.
               Office of Cancer Genomics
               National Cancer Institute / NIH
               Bldg. 31 Rm10A07 Bethesda, MD 20892
               Email: cgapbs-r@mail.nih.gov
               Tissue Procurement: GPCR Consortium
                cDNA Library Preparation: GPCR Consortium
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: Agencourt Bioscience Corporation
                Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               http://image.llnl.gov
               Plate: IRBI02 row: a column: 09
               High quality sequence start: 9
               High quality sequence stop: 772.
FEATURES   Location/Qualifiers
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                     /clone="IMAGE:6971890"
                     /tissue_type="mixed"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_145"
                     /note="Vector: pcDNA3.1; Site_1: varies by clone; Site_2:
                     varies by clone; ORFs were PCR-amplified and cloned into
                     pcDNA3.1 by the GPCR Consortium. Cloning sites vary by
                     clone and include the following: 5'-EcoRV-XmnI/XhoI-3',
                     5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).
                     For information about which gene each clones represents,
                     please visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBI.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

     Query Match   32.4%; Score 367; DB 14; Length 788;
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Best Local Similarity   72.7%;   Pred. No. 2.8e-66;
Matches 472; Conservative   0; Mismatches 177; Indels   0; Gaps   0;

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Qy        80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
             | || || || || || || || |||||| | || || ||| |||| ||| | |||||||
Db       140 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTGCACCCGAAAGAATATGAGT 199

Qy       140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
             |||·||||| ||||| | || |      |||||||||||||||| || | || |||  ||||
Db       200 GGGTCCTGATCGCCGGGTACATCATCGTGTTCGTCGTGGCTCTCATTGGGAACGTCCTGG 259

Qy       200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
             | || |||| |||||| |||||| |||||||||||||||||||| || |||||||||||| ||||
Db       260 TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA 319

Qy       260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
             | || || ||||||||| || || |||||     | |||||| || |||| ||| | ||||
Db       320 ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCCAGCCACACTGGTCGTGG 379

Qy       320 ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG 379
             | |||||| ||| |||||| | || || || |||·| ||||| || || || ||||||||||
Db       380 ATATCACCGAGACCTGGTTTTTTGGACAGTCCCTTTGCAAAGTGATTCCTTATCTACAGA 439

Qy       380 CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATG 439
             | |||||| ||||| ||| | | || || || || |||| |||||| |||| || ||||||||
Db       440 CCGTGTCGGTGTCTGTGTCTGTCCTCACACTGAGCTGTATCGCCTTGGATCGGTGGTATG 499

Qy       440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG 499
             | |||||| ||||| |    |||| |||||||||| |||||||| | || |
Db       500 CAATCTGTCACCCTTTGATGTTTAAGAGCACAGCAAAGCGGGCCCGTAACAGCATTGTCA 559

Qy       500 GCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCA 559
             ||||||| ||| || || ||| | || |||||     |||||||| |||||||
Db       560 TCATCTGGATTGTCTCCTGCATTATAATGATTCCTCAGGCCATCGTCATGGAGTGCAGCA 619

Qy       560 GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGG 619
             |||| | || | ||||||| ||      ||||| | || |||||||||| |||||||
Db       620 CTGTGTTCCCAGGCTTAGCCAATAAAACCACCCTCTTTACGGTGTGTGATGAGCGCTGGG 679

Qy       620 CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCC 679
             | ||| | ||||||||||| ||||||| || ||||||| | || || ||| |||| |
Db       680 GTGGTGAAATTTATCCCAAGATGTACCACATCTGTTTCTTTCTGGTGACATACATGGCAC 739

Qy       680 CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTG 728
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Db       740 CACTGTGTCTCATGGTGTTGGCTTATCTGNCAATATTCGCANACTCTG 788
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Search completed: October 15, 2004, 22:50:33
Job time : 3299.03 secs

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                        GenCore version 5.1.6
              Copyright (c) 1993 - 2004  Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:          October 15, 2004, 13:54:41 ; Search time 4590.56 Seconds
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Title:           US-10-070-532-5
Perfect score:   1133
Sequence:        1 atggagccctcagccacccc..........tcctgaccatcgtgccccgg 1133

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters:      6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       GenEmbl:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1131.4	99.9	1133	6	E43973	E43973 Novel G pro
2	1131.4	99.9	1133	6	AX746120	AX746120 Sequence
3	1131.4	99.9	1133	6	BD185454	BD185454 Human neu
4	1128.2	99.6	1170	6	E43972	E43972 Novel G pro
5	1128.2	99.6	1170	6	AX746118	AX746118 Sequence
6	1114.4	98.4	1116	6	AR216119	AR216119 Sequence
7	1086.4	95.9	1209	6	AR216117	AR216117 Sequence
8	1086.4	95.9	1564	6	E43974	E43974 Novel G pro
9	1086.4	95.9	1564	6	E50810	E50810 Novel G pro
10	1086.4	95.9	1564	6	E50811	E50811 Novel G pro
11	1086.4	95.9	1564	6	AX299473	AX299473 Sequence
12	1086.4	95.9	1564	6	AX299475	AX299475 Sequence
13	1086.4	95.9	1564	6	AX549082	AX549082 Sequence
14	1086.4	95.9	1564	6	AX746121	AX746121 Sequence
15	1086.4	95.9	1564	6	AX840912	AX840912 Sequence
16	1086.4	95.9	1564	9	AF041243	AF041243 Homo sapi
17	1084.8	95.7	1110	6	AR216118	AR216118 Sequence
18	1081.6	95.5	1209	6	BD185452	BD185452 Human neu
19	1081.6	95.5	1278	6	AX280925	AX280925 Sequence
20	1076.8	95.0	1110	6	BD185453	BD185453 Human neu
21	892.8	78.8	2200	10	AY336083	AY336083 Mus muscu
22	891.2	78.7	2469	10	AF041244	AF041244 Rattus no
23	697.6	61.6	843	6	AR109899	AR109899 Sequence
24	670.6	59.2	789	6	AR109632	AR109632 Sequence
25	670.6	59.2	789	6	E12154	E12154 cDNA encodi
26	670.6	59.2	789	6	AR300942	AR300942 Sequence
27	579.6	51.2	781	10	AF394596	AF394596 Mus muscu
28	554.4	48.9	3114	10	AF041246	AF041246 Rattus no
29	530.4	46.8	1545	10	AY336084	AY336084 Mus muscu
30	530.4	46.8	2117	10	AY336085	AY336085 Mus muscu
31	520.8	46.0	1633	6	E33974	E33974 cDNA clone
32	520.8	46.0	1843	6	AX549084	AX549084 Sequence
33	520.8	46.0	1843	6	AX840914	AX840914 Sequence

34	520.8	46.0	1878	9	AF041245	AF041245 Homo sapi
35	516	45.5	1335	6	AX280927	AX280927 Sequence
36	514.4	45.4	1805	4	AF164626	AF164626 Canis fam
37	496.2	43.8	597	10	AY255599	AY255599 Mus muscu
38	329.2	29.1	382	4	AF499612	AF499612 Ovis arie
39	304.2	26.8	637	10	AF394597	AF394597 Mus muscu
40	281.6	24.9	328	4	AB092488	AB092488 Bos tauru
41	263.2	23.2	501	4	AF532967	AF532967 Ovis arie
42	249.2	22.0	344	9	F202078S03	AF202080 Homo sapi
43	249.2	22.0	9785	6	AR178605	AR178605 Sequence
44	249.2	22.0	9785	6	AX088174	AX088174 Sequence
45	249.2	22.0	9785	9	AY062030	AY062030 Homo sapi

ALIGNMENTS

RESULT 1
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LOCUS   E43973   1133 bp   DNA   linear   PAT 31-JAN-2002
DEFINITION   Novel G protein-coupled receptor (HFGAN72Y).
ACCESSION   E43973
VERSION   E43973.1 GI:18625172
KEYWORDS   JP 2000106888-A/2.
SOURCE   unidentified
  ORGANISM   unidentified
                unclassified.
REFERENCE   1 (bases 1 to 1133)
  AUTHORS   Bergsma,D.J. and Ellis,C.E.
  TITLE   Novel G protein-coupled receptor (HFGAN72Y)
  JOURNAL   Patent: JP 2000106888-A 2 18-APR-2000;
                SMITHKLINE BEECHAM CORP
COMMENT   OS   Unidentified
                PN   JP 2000106888-A/2
                PD   18-APR-2000
                PF   21-JUL-1999 JP 1999206116
                PR   30-APR-1997 US   08/846705
                PI   DERK J BERGSMA,CATHARINE ELIZABETH ELLIS
                PC   C12N15/09,A61K38/00,A61K38/00,A61K45/00,A61K48/00,A61P1/00, PC
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                PC   A61P9/02,A61P9/04,A61P9/10,A61P9/12,A61P11/06,A61P13/02, PC
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                PC   A61P19/10,A61P25/14,A61P25/16,A61P25/18,A61P25/22,A61P25/24,
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                PC   A61P43/00,
                PC   C07K14/705,C07K16/28,C12N1/21,C12N5/10,C12P21/02,G01N33/566,
                PC   G01N33/577//
                PC   C12P21/08,(C12N15/09,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,
                PC   A61K37/02,
                PC   A61K37/02,C12N5/00,(C12N15/00,C12R1:91)
                CC   Strandedness: Single;
                CC   Topology: Linear;
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FEATURES   Location/Qualifiers

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ORIGIN

  Query Match            99.9%;   Score 1131.4;   DB 6;   Length 1133;
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  Matches 1132;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;


Qy        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
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Db        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Qy      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Qy      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Qy      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy      541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy      601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy      661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Qy       1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG 1133
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RESULT 2
AX746120

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LOCUS       AX746120                1133 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 3 from Patent EP1156110.
ACCESSION   AX746120
VERSION     AX746120.1  GI:31744926
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Bergsma,D.J. and Ellis,C.E.
  TITLE     G-protein coupled receptor (HFGAN72Y)
  JOURNAL   Patent: EP 1156110-A 3 21-NOV-2001;
            SMITHKLINE BEECHAM CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .1133
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                     /db_xref="taxon:9606"
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ORIGIN
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Query Match              99.9%;  Score 1131.4;  DB 6;  Length 1133;
Best Local Similarity    99.9%;  Pred. No. 2.2e-218;
Matches 1132;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;
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Qy     1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
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Qy    61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Qy   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Qy   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Qy   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy   301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Db   301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy   361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Qy   481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Qy   601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Qy   661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Db   661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy   721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy   781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Db     841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy     901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
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Db     901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy     961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Qy    1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Qy    1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG 1133
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RESULT 3
BD185454
LOCUS       BD185454                 1133 bp     DNA        linear     PAT 17-JUN-2003
DEFINITION  Human neuropeptide receptor.
ACCESSION   BD185454
VERSION     BD185454.1  GI:31877654
KEYWORDS    JP 2002360288-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1133)
  AUTHORS   Soppet,D.R., Li,Y. and Rosen,C.A.
  TITLE     Human neuropeptide receptor
  JOURNAL   Patent: JP 2002360288-A 3 17-DEC-2002;
            HUMAN GENOME SCIENCES INC
COMMENT     OS   Unidentified
            PN   JP 2002360288-A/3
            PD   17-DEC-2002
            PF   02-MAY-2002 JP 2002130838
            PI   DANIEL R SOPPET,YI LI,CRAIG A ROSEN
            PC   C12N15/09,A61K31/7088,A61K38/00,A61K45/00,A61K48/00,A61P3/04,
            PC   A61P3/06,
            PC   A61P3/10,A61P9/10,A61P9/12,A61P25/08,A61P25/18,A61P25/22, PC
            A61P25/28,
            PC   A61P35/00,A61P43/00,C07K14/705,C07K16/24,C12N1/15,C12N1/19, PC
              C12N1/21,
            PC   C12N5/10,C12Q1/68,C12N15/00,C12N5/00,A61K37/02 CC
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            CC   Topology: Linear;
            CC   Human neuropeptide receptor
            FH   Key             Location/Qualifiers
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            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
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                     /organism="unidentified"
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ORIGIN

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Query Match           99.9%;   Score 1131.4;  DB 6;   Length 1133;
Best Local Similarity 99.9%;   Pred. No. 2.2e-218;
Matches 1132;  Conservative   0;  Mismatches    1;  Indels   0;  Gaps    0;


Qy       1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
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Db       1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGACCC 60


Qy      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120


Qy     121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Qy     181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Qy     241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Qy     301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Qy     481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Qy     601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Qy     661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Qy    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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Db    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy    841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Db    841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy    901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
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Db    901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy    961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Qy   1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG 1133
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RESULT 4
E43972
LOCUS       E43972                  1170 bp    DNA     linear    PAT 31-JAN-2002
DEFINITION  Novel G protein-coupled receptor (HFGAN72Y).
ACCESSION   E43972
VERSION     E43972.1  GI:18625171
KEYWORDS    JP 2000106888-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1170)
  AUTHORS   Bergsma,D.J. and Ellis,C.E.
  TITLE     Novel G protein-coupled receptor (HFGAN72Y)
  JOURNAL   Patent: JP 2000106888-A 1 18-APR-2000;
            SMITHKLINE BEECHAM CORP
COMMENT     OS   Unidentified
            PN   JP 2000106888-A/1
            PD   18-APR-2000
            PF   21-JUL-1999 JP 1999206116
            PR   30-APR-1997 US    08/846705
            PI   DERK J BERGSMA,CATHARINE ELIZABETH ELLIS
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            PC   A61P9/02,A61P9/04,A61P9/10,A61P9/12,A61P11/06,A61P13/02, PC
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            PC   A61P19/10,A61P25/14,A61P25/16,A61P25/18,A61P25/22,A61P25/24,
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        PC    G01N33/577//
        PC    C12P21/08,(C12N15/09,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,
        PC    A61K37/02,
        PC    A61K37/02,C12N5/00,(C12N15/00,C12R1:91)
        CC    Strandedness: Single;
        CC    Topology: Linear;
        FH    Key             Location/Qualifiers
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        FT                    /organism='Unidentified'.
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  Query Match              99.6%;   Score 1128.2;   DB 6;   Length 1170;
  Best Local Similarity    99.7%;   Pred. No. 9.6e-218;
  Matches 1130;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;


Qy         1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
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Qy        61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Qy       121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Qy       301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Db       361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy       421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db       421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy       481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Db      541  GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA  600

Qy      601  GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT  660
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Db      601  GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT  660

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Db      661  ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC  720

Qy      721  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC  780
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Qy      781  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC  840
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Db      781  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC  840

Qy      841  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG  900
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Db      841  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG  900

Qy      901  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT  960
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Db      901  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT  960

Qy      961  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC  1020

Qy     1021  ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC  1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021  ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC  1080

Qy     1081  CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG  1133
             ||||||||||||||||||||||||||||||  ||||||||  ||||||||||||
Db     1081  CTCAGTGGATGTAAAGAGAAGAGTCTAGCTCTGTCCTGCCCATCGTGCCCCGG  1133
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RESULT 5
AX746118
LOCUS          AX746118                 1170 bp    DNA       linear    PAT 12-JUN-2003
DEFINITION     Sequence 1 from Patent EP1156110.
ACCESSION      AX746118
VERSION        AX746118.1  GI:31744924
KEYWORDS       .
SOURCE         Homo sapiens (human)
  ORGANISM     Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
  AUTHORS      Bergsma,D.J. and Ellis,C.E.
  TITLE        G-protein coupled receptor (HFGAN72Y)
  JOURNAL      Patent: EP 1156110-A 1 21-NOV-2001;
               SMITHKLINE BEECHAM CORPORATION (US)
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FEATURES             Location/Qualifiers
     source          1. .1170
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            1. .1170
                     /gene="HFGAN72Y"
     CDS             1. .1170
                     /gene="HFGAN72Y"
                     /codon_start=1
                     /protein_id="CAD97474.1"
                     /db_xref="GI:31744925"
                     /translation="MEPSATPGAQMGVPPGSREPSPVPPDYEDEFLRYLWRDYLYPKQ
                     YEWVLIAAYVAVFVVALVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPA
                     SLLVDITESWLFGHALCKVIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARR
                     ARGSILGIWAVSLAIMVPQAAVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSC
                     FFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSALVRNWKRPSDQLGDLEQGLSGEP
                     QPRGRAFLAEVKQMRARRKTAKMLMVVLLVFALCYLPISVLNVLKRVFGMFRQASDRE
                     AVYACFTFSHWLVYANSAANPIIYNFLSGCKEKSLALSCPSCPGHDPHLAAALCS"
ORIGIN
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Query Match	99.6%;	Score 1128.2; DB 6; Length 1170;
Best Local Similarity	99.7%;	Pred. No. 9.6e-218;
Matches 1130; Conservative	0;	Mismatches 3; Indels 0; Gaps 0;

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Qy        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy      301 CCGGCCAGCCTCCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy      421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db      421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Qy    481  GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
           ·· ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy    541  GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Db    541  GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy    601  GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db    601  GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy    661  ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy    721  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy    781  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy    841  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy    901  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy    961  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy   1021  ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Db   1021  ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy   1081  CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG 1133
           |||||||||||||||||||||||||||| ||||||||| |||||||||||||
Db   1081  CTCAGTGGATGTAAAGAGAAGAGTCTAGCTCTGTCCTGCCCATCGTGCCCCGG 1133
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RESULT 6
AR216119
LOCUS   AR216119   1116 bp   DNA   linear   PAT 25-SEP-2002
DEFINITION Sequence 5 from patent US 6410701.
ACCESSION   AR216119
VERSION   AR216119.1 GI:23314432
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1116)
  AUTHORS   Soppet,D.R., Li,Y. and Rosen,C.A.

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   TITLE      Human neuropeptide receptor
  JOURNAL     Patent: US 6410701-A 5 25-JUN-2002;
 FEATURES             Location/Qualifiers
    source           1. .1116
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

   Query Match            98.4%;   Score 1114.4;  DB 6;   Length 1116;
   Best Local Similarity  99.9%;   Pred. No. 5.9e-215;
   Matches 1115;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;


Qy        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGACCCC 60


Qy       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120


Qy      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180


Qy      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240


Qy      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300


Qy      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Db      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360


Qy      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420


Qy      421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480


Qy      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Db      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540


Qy      541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Db      541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600


Qy      601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Qy      661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy       721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy       781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy       841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy       901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy       961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCC 1116
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCC 1116



RESULT 7
AR216117
LOCUS       AR216117                1209 bp    DNA        linear    PAT 25-SEP-2002
DEFINITION  Sequence 1 from patent US 6410701.
ACCESSION   AR216117
VERSION     AR216117.1  GI:23314430
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1209)
  AUTHORS   Soppet,D.R., Li,Y. and Rosen,C.A.
  TITLE     Human neuropeptide receptor
  JOURNAL   Patent: US 6410701-A 1 25-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .1209
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

   Query Match         95.9%;   Score 1086.4;  DB 6;  Length 1209;
   Best Local Similarity   99.9%;   Pred. No. 2.7e-209;
   Matches 1087;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG  60

Qy    61  TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy   121  TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy   181  CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy   241  ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db   241  ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy   301  CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy   361  GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy   421  GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy   481  GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy   541  GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Db   541  GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy   601  GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db   601  GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy   661  ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATCCGC 720

Qy   721  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy   781  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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Db   781  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy   841  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy       901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy       961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy      1081 CTCAGTGG 1088
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Db      1081 CTCAGTGG 1088
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RESULT 8
E43974
LOCUS   E43974   1564 bp   DNA   linear   PAT 31-JAN-2002
DEFINITION Novel G protein-coupled receptor (HFGAN72Y).
ACCESSION   E43974
VERSION   E43974.1 GI:18625173
KEYWORDS   JP 2000106888-A/3.
SOURCE   unidentified
  ORGANISM unidentified
            unclassified.
REFERENCE   1 (bases 1 to 1564)
  AUTHORS   Bergsma,D.J. and Ellis,C.E.
  TITLE   Novel G protein-coupled receptor (HFGAN72Y)
  JOURNAL   Patent: JP 2000106888-A 3 18-APR-2000;
            SMITHKLINE BEECHAM CORP
COMMENT   OS   Unidentified
            PN   JP 2000106888-A/3
            PD   18-APR-2000
            PF   21-JUL-1999 JP 1999206116
            PR   30-APR-1997 US   08/846705
            PI   DERK J BERGSMA,CATHARINE ELIZABETH ELLIS
            PC   C12N15/09,A61K38/00,A61K38/00,A61K45/00,A61K48/00,A61P1/00, PC
              A61P1/14,
            PC   A61P9/02,A61P9/04,A61P9/10,A61P9/12,A61P11/06,A61P13/02, PC
            A61P13/08,
            PC   A61P19/10,A61P25/14,A61P25/16,A61P25/18,A61P25/22,A61P25/24,
            PC   A61P31/04,
            PC   A61P31/10,A61P31/12,A61P31/18,A61P33/00,A61P35/00,A61P37/08,
            PC   A61P43/00,
            PC   C07K14/705,C07K16/28,C12N1/21,C12N5/10,C12P21/02,G01N33/566,
            PC   G01N33/577//
            PC   C12P21/08,(C12N15/09,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,
            PC   A61K37/02,
            PC   A61K37/02,C12N5/00,(C12N15/00,C12R1:91)
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key   Location/Qualifiers
            FT   source   1. .1564

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   Query Match            95.9%;  Score 1086.4;  DB 6;  Length 1564;
   Best Local Similarity  99.9%;  Pred. No. 2.6e-209;
   Matches 1087;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;


Qy        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
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Db      154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db      214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Db      274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db      334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Db      454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy      421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db      574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Db      634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy      541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Db      694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy      601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db      754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy      661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Db     814    ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC    873

Qy     721    AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC    780
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     874    AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC    933

Qy     781    CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC    840
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     934    CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC    993

Qy     841    CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG    900
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Db     994    CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG    1053

Qy     901    ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT    960
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     1054   ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT    1113

Qy     961    AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC    1020
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Db     1114   AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC    1173

Qy     1021   ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC    1080
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     1174   ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC    1233

Qy     1081   CTCAGTGG    1088
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Db     1234   CTCAGTGG    1241
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RESULT 9
E50810
LOCUS   E50810   1564 bp   DNA   linear   PAT 18-JUN-2001
DEFINITION   Novel G protein-bound receptor (HFGAN 72X).
ACCESSION   E50810
VERSION   E50810.1 GI:13023197
KEYWORDS   JP 2000060578-A/1.
SOURCE   unidentified
  ORGANISM   unidentified
               unclassified.
REFERENCE   1 (bases 1 to 1564)
  AUTHORS   Derk,J.B. and Catharine,E.E.
  TITLE   Novel G protein-bound receptor (HFGAN 72X)
  JOURNAL   Patent: JP 2000060578-A 1 29-FEB-2000;
               SMITHKLINE BEECHAM CORP
COMMENT   OS   Unidentified
               PN   JP 2000060578-A/1
               PD   29-FEB-2000
               PF   21-JUL-1999 JP 1999206115
               PR   30-APR-1997 US   08/846704
               PI   DERK J BERGSMA,CATHARINE ELIZABETH ELLIS
               PC   C12N15/09,A61K31/70,A61K38/00,A61K39/00,A61K39/395,A61K39/395,
               PC   A61K45/00,
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          PC    A61P35/00,A61P37/00,C07K14/705,C12N5/10,C12P21/02,C12Q1/02, PC
            G01N33/53,
          PC    G01N33/566//C07K16/28,C12N15/00,A61K37/02,C12N5/00 CC
          Strandedness: Single;
          CC    Topology: Linear;
          FH    Key              Location/Qualifiers
          FT    source           1. .1564
          FT                     /organism='Unidentified'.
FEATURES             Location/Qualifiers
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  Query Match              95.9%;  Score 1086.4;  DB 6;  Length 1564;
  Best Local Similarity    99.9%;  Pred. No. 2.6e-209;
  Matches 1087;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;


Qy      1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db    214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy    121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db    334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db    394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Db    514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Db    634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693
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Qy     541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Db     694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy     601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db     754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy     661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Db     814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy     721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy     781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy     841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy     901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy     961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy    1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy    1081 CTCAGTGG 1088
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Db    1234 CTCAGTGG 1241


RESULT 10
E50811
LOCUS       E50811                   1564 bp    DNA      linear    PAT 18-JUN-2001
DEFINITION  Novel G protein-bound receptor (HFGAN 72X).
ACCESSION   E50811
VERSION     E50811.1  GI:13023198
KEYWORDS    JP 2000060578-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1564)
  AUTHORS   Derk,J.B. and Catharine,E.E.
  TITLE     Novel G protein-bound receptor (HFGAN 72X)
  JOURNAL   Patent: JP 2000060578-A 2 29-FEB-2000;
            SMITHKLINE BEECHAM CORP
COMMENT     OS   Unidentified
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FEATURES   Location/Qualifiers
     source   1. .1564
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                  /db_xref="taxon:32644"

ORIGIN

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 Query Match           95.9%;  Score 1086.4;  DB 6;  Length 1564;
 Best Local Similarity 99.9%;  Pred. No. 2.6e-209;
 Matches 1087; Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;


Qy      1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213


Qy     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273


Qy    121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333


Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db    334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393


Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453


Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Db    454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513


Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Qy        421  GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db        574  GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy        481  GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Db        634  GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy        541  GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Db        694  GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy        601  GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db        754  GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy        661  ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814  ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy        721  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Db        874  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy        781  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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Db        934  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy        841  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy        901  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
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Db       1054  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy        961  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021  ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Db       1174  ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081  CTCAGTGG 1088
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Db       1234  CTCAGTGG 1241
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RESULT 11
AX299473
LOCUS   AX299473   1564 bp   DNA   linear   PAT 26-NOV-2001
DEFINITION   Sequence 1 from Patent EP1154019.
ACCESSION   AX299473
VERSION   AX299473.1 GI:17129230
KEYWORDS   .

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  Query Match              95.9%;   Score 1086.4;   DB 6;   Length 1564;
  Best Local Similarity    99.9%;   Pred. No. 2.6e-209;
  Matches 1087;  Conservative     0;  Mismatches      1;  Indels    0;  Gaps      0;


Qy        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
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Db      154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213


Qy       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db      214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273


Qy      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Db      274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333


Qy      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393


Qy      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453


Qy      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Db      454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513


Qy      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
            ||||||||||||||||||||||||||||||||||||TT||||||||||||||||||||||||
Db      514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573


Qy      421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633


Qy      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693


Qy      541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Db     694    GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy     601    GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     754    GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy     661    ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     814    ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy     721    AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     874    AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy     781    CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     934    CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy     841    CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     994    CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy     901    ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1054   ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy     961    AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1114   AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy     1021   ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1174   ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy     1081   CTCAGTGG 1088
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Db     1234   CTCAGTGG 1241
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RESULT 12
AX299475
LOCUS   AX299475   1564 bp   DNA   linear   PAT 26-NOV-2001
DEFINITION   Sequence 3 from Patent EP1154019.
ACCESSION   AX299475
VERSION   AX299475.1 GI:17129231
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Bergsma,D.J. and Ellis,C.E.
  TITLE   G-protein coupled receptor (hfgan72x)
  JOURNAL   Patent: EP 1154019-A 3 14-NOV-2001;
               SmithKline Beecham Corporation (US)
FEATURES   Location/Qualifiers

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        source              1. .1564
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                            /mol_type="unassigned DNA"
                            /db_xref="taxon:9606"
      ORIGIN

       Query Match              95.9%;   Score 1086.4;   DB 6;   Length 1564;
       Best Local Similarity    99.9%;   Pred. No. 2.6e-209;
       Matches 1087;  Conservative    0;  Mismatches    1;   Indels    0;   Gaps    0;


     Qy        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     Db      154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

     Qy       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     Db      214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

     Qy      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     Db      274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

     Qy      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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     Db      334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

     Qy      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     Db      394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

     Qy      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     Db      454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

     Qy      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     Db      514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

     Qy      421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     Db      574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

     Qy      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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     Db      634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

     Qy      541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACGCACACGGCTCTTCTCA 600
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     Db      694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACGCACACGGCTCTTCTCA 753

     Qy      601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     Db      754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

     Qy      661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     Db      814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873
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Qy       721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Db       874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy       781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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Db       934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy       841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Db       994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy       901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy       961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy      1081 CTCAGTGG 1088
             ||||||||
Db      1234 CTCAGTGG 1241


RESULT 13
AX549082
LOCUS       AX549082                1564 bp    DNA        linear    PAT 26-NOV-2002
DEFINITION  Sequence 367 from Patent WO02061087.
ACCESSION   AX549082
VERSION     AX549082.1  GI:25813851
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Burmer,G.C., Roush,C.L. and Brown,J.P.
  TITLE     Antigenic peptides, such as for G protein-coupled receptors
            (GPCRs), antibodies thereto, and systems for identifying such
            antigenic peptides
  JOURNAL   Patent: WO 02061087-A 367 08-AUG-2002;
            Lifespan Biosciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1564
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match            95.9%;  Score 1086.4;  DB 6;  Length 1564;
  Best Local Similarity  99.9%;  Pred. No. 2.6e-209;
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      Matches 1087;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Db      274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db      334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
            ||||||||||||||.|||||||||||||||||||||||||||||||||||||||||||||
Db      514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy      421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db      574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Db      634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy      541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Db      694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy      601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy      661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Db      814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy      721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Db      874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy      781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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Db      934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993
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Qy      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Db      994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy     1081 CTCAGTGG 1088
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Db     1234 CTCAGTGG 1241
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RESULT 14
AX746121

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LOCUS       AX746121                1564 bp    DNA        linear    PAT 12-JUN-2003
DEFINITION  Sequence 4 from Patent EP1156110.
ACCESSION   AX746121
VERSION     AX746121.1  GI:31744927
KEYWORDS     .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Bergsma,D.J. and Ellis,C.E.
  TITLE     G-protein coupled receptor (HFGAN72Y)
  JOURNAL   Patent: EP 1156110-A 4 21-NOV-2001;
            SMITHKLINE BEECHAM CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .1564
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /note="HGS EST 554692"
ORIGIN
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  Query Match            95.9%;  Score 1086.4;  DB 6;  Length 1564;
  Best Local Similarity  99.9%;  Pred. No. 2.6e-209;
  Matches 1087;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
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Db      154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db      214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273
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Qy    121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db    334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db    394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Db    454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Qy    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Db    874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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Db    934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy    841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Db    994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy    901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113
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Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081 CTCAGTGG 1088
              ||||||||
Db       1234 CTCAGTGG 1241
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RESULT 15
AX840912

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LOCUS       AX840912                1564 bp    DNA        linear   PAT 16-DEC-2003
DEFINITION  Sequence 8 from Patent WO03075945.
ACCESSION   AX840912
VERSION     AX840912.1  GI:39979051
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Eulenberg,K., Steuernagel,A., Haeder,T. and Broenner,G.
  TITLE     Cg8327, cg10823, cg18418, cg15862, cg3768, cg11447 and cg16750
            homologous proteins involved in the regulation of energy
            homeostasis
  JOURNAL   Patent: WO 03075945-A 8 18-SEP-2003;
            DeveloGen Aktiengesellschaft fuer entwicklungsbiologische;
            Forschung (DE)
FEATURES             Location/Qualifiers
     source          1. .1564
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN
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  Query Match          95.9%;   Score 1086.4;   DB 6;   Length 1564;
  Best Local Similarity  99.9%;   Pred. No. 2.6e-209;
  Matches 1087;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;
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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db      334  CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC  393

Qy      241  ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      394  ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG  453

Qy      301  CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG  360
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Db      454  CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG  513

Qy      361  GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      514  GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC  573

Qy      421  GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG  480
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Db      574  GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG  633

Qy      481  GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      634  GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT  693

Qy      541  GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA  600
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Db      694  GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA  753

Qy      601  GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT  660
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Db      754  GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT  813

Qy      661  ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      814  ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC  873

Qy      721  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC  780
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Db      874  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC  933

Qy      781  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC  840
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Db      934  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC  993

Qy      841  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG  900
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Db      994  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG  1053

Qy      901  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT  960
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Db      1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT  1113

Qy      961  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC  1173

Qy      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC  1080
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Db      1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC  1233
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Qy       1081 CTCAGTGG 1088
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Db       1234 CTCAGTGG 1241


Search completed: October 15, 2004, 19:59:40
Job time : 4593.56 secs
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OM nucleic - nucleic search, using sw model

Run on: October 15, 2004, 13:52:46 ; Search time 483.963 Seconds
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Perfect score: 1133
Sequence: 1 atggagccctcagccacccc..........tcctgaccatcgtgccccgg 1133

Scoring table: IDENTITY_NUC
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Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                   SUMMARIES

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1	1133	100.0	1133	4	AAS00493	Aas00493 Human neu
2	1131.4	99.9	1133	2	AAT42828	Aat42828 Neuropept
3	1131.4	99.9	1133	2	AAV68512	Aav68512 Nucleotid
4	1131.4	99.9	1133	6	ABA96020	Aba96020 HGS EST 5
5	1128.2	99.6	1170	2	AAV68511	Aav68511 Nucleotid
6	1128.2	99.6	1170	6	ABA96019	Aba96019 G-protein
7	1086.4	95.9	1564	2	AAV63468	Aav63468 cDNA enco

8	1086.4	95.9	1564	2	AAV68514		Aav68514	Nucleotid
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11	1086.4	95.9	1564	6	AAI64173		Aai64173	HFGAN72X
12	1086.4	95.9	1564	6	AAI64172		Aai64172	Human HFG
13	1086.4	95.9	1564	7	ABZ42789		Abz42789	Human ore
14	1084.8	95.7	1110	2	AAT42827		Aat42827	Neuropept
15	1084.8	95.7	1278	4	AAS00491		Aas00491	Human neu
16	1084.8	95.7	1564	4	AAS17464		Aas17464	Human G p
17	1083.2	95.6	1209	2	AAT42826		Aat42826	Neuropept
18	1081.6	95.5	1278	5	ABI98014		Abi98014	Non-endog
19	1076.8	95.0	1110	4	AAS00492		Aas00492	Human neu
20	1040	91.8	1278	4	AAD09335		Aad09335	Cynomolgo
21	912	80.5	1281	5	AAC85974		Aac85974	Dog orexi
22	670.6	59.2	789	2	AAT13909		Aat13909	Rabbit G-
23	670.6	59.2	789	2	AAT51065		Aat51065	G-protein
24	520.8	46.0	1633	2	AAX29700		Aax29700	Human 7-t
25	520.8	46.0	1843	7	ABZ42790		Abz42790	Human ore
26	516.2	45.6	1335	4	AAF90300		Aaf90300	Nucleotid
27	516	45.5	1335	5	ABI98015		Abi98015	Non-endog
28	249.2	22.0	344	5	AAF56748		Aaf56748	Human HCR
29	249.2	22.0	9785	5	AAF55159		Aaf55159	Nucleotid
30	249.2	22.0	10453	4	AAS17462		Aas17462	Human G p
31	244	21.5	244	4	AAS17449		Aas17449	Human G p
32	230	20.3	331	5	AAF56750		Aaf56750	Human HCR
33	225.4	19.9	227	4	AAS17453		Aas17453	Human G p
34	197.4	17.4	356	4	AAS17445		Aas17445	Human G p
35	197	17.4	452	5	AAF56746		Aaf56746	Human HCR
36	181	16.0	263	5	AAF56747		Aaf56747	Human HCR
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38	163.2	14.4	1290	3	AAA70507		Aaa70507	Novel hum
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40	163.2	14.4	1290	4	AAH78518		Aah78518	Nucleotid
41	163.2	14.4	1290	4	AAH78519		Aah78519	Nucleotid
42	163.2	14.4	1290	7	ACC49315		Acc49315	Human RFR
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44	163.2	14.4	1290	9	ADB76179		Adb76179	Altenativ
45	163.2	14.4	1290	9	ADB76178		Adb76178	Human OT7

ALIGNMENTS

RESULT 1
AAS00493
ID   AAS00493 standard; cDNA; 1133 BP.
XX
AC   AAS00493;
XX
DT   17-MAY-2001 (first entry)
XX
DE   Human neuropeptide receptor splice variant 2 cDNA.
XX
KW   Human; neuropeptide receptor; neuropeptide Y receptor; obesity;
KW   nervous system disorder; hyperproliferative disorder; diabetes mellitus;
KW   cardiovascular disorder; autoimmune disorder; infectious disorder;
KW   eating behaviour disorder; narcolepsy; neurological disease;

      Query Match   100.0%;   Score 1133;   DB 4;   Length 1133;
      Best Local Similarity 100.0%;   Pred. No. 1.8e-263;
      Matches 1133; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60

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Db        1  ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC  60

Qy       61  TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61  TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy      121  TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Db      121  TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy      181  CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db      181  CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy      241  ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db      241  ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy      301  CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Db      301  CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy      361  GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Db      361  GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy      421  GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db      481  GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy      541  GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Db      541  GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy      601  GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db      601  GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy      661  ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Qy      721  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Db      721  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy      781  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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Qy      841  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
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Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG 1133
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG 1133
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RESULT 2
AAT42828
ID   AAT42828 standard; cDNA; 1133 BP.
XX
AC   AAT42828;
XX
DT   22-FEB-1997   (first entry)
XX
DE   Neuropeptide receptor splice variant-2 gene.
XX
KW   Human; neuropeptide receptor; splice variant; drug screening;
KW   receptor-agonist; receptor-antagonist; anorectic; antitumour;
KW   anticholesterolemic; neuroprotective; anticonvulsant; hypotensive;
KW   sedative; diagnostic; gene therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   misc_feature   1117. .1119
FT   /*tag= a
FT   /note= "In-frame stop codon"
XX
PN   WO9634877-A1.
XX
PD   07-NOV-1996.
XX
PF   05-MAY-1995;   95WO-US005616.
XX
PR   05-MAY-1995;   95WO-US005616.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Soppet DR, Li Y, Rosen CA;
XX
DR   WPI; 1996-506094/50.
DR   P-PSDB; AAW06126.
XX
PT   Human neuro-peptide receptor polypeptide(s) - used to identify
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PT   antagonists and agonists to such polypeptide(s), e.g. in the treatment of
PT   obesity, Alzheimer's disease, epilepsy, etc. .
XX
PS   Disclosure; Page 52; 77pp; English.
XX
CC   The sequence encodes human neuropeptide receptor splice variant-2, which
CC   retains activity corresponding to the mature receptor (encoded by
CC   AAT42826). The receptor gene has been isolated from from a human adult
CC   hypothalamus cDNA library, and is structurally related to the G-protein-
CC   coupled receptor family. The receptor may be used in a drug screening
CC   assay for isolation of receptor-agonists and -antagonists, which may be
CC   used as anorectic, antitumour, anticholesterolemic, neuroprotective,
CC   anticonvulsant, hypotensive or sedative drugs, etc. The DNA may also be
CC   used in genetic disease diagnosis or gene therapy. The receptor and its
CC   corresponding antibody may also be used in therapy and diagnosis
XX
SQ   Sequence 1133 BP; 202 A; 368 C; 312 G; 251 T; 0 U; 0 Other;
```

    Query Match   99.9%;   Score 1131.4;   DB 2;   Length 1133;
    Best Local Similarity   99.9%;   Pred. No. 4.5e-263;
    Matches 1132;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

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Qy      1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
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Db      1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGACCCC 60

Qy     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy    121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Db    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
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Db	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600

Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
		||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||	
Db	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660

Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
		||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||	
Db	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720

Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC	780
		||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||	
Db	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC	780

Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
		||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||	
Db	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840

Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
		||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||	
Db	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900

Qy	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
		||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||	
Db	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960

Qy	961	AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
		||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||	
Db	961	AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020

Qy	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC	1080
		||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||	
Db	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC	1080

Qy	1081	CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG	1133
		||||||||||||||||||||||||||||||||||||||||||||||||||||	
Db	1081	CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG	1133

RESULT 3
AAV68512
ID   AAV68512 standard; cDNA; 1133 BP.
XX
AC   AAV68512;
XX
DT   29-JAN-1999 (first entry)
XX
DE   Nucleotide sequence of HGS EST 557082.
XX
KW   HGS EST 557082; G-protein coupled receptor family; HFGAN72Y; mutation;
KW   probe; agonist; antagonist; activation; inhibition; gene therapy;
KW   antibody; immune response; vaccine; HIV-1; HIV-2; cancer; anorexia;
KW   bulimia; asthma; Parkinson's disease; acute heart failure; hypotension;
KW   hypertension; urinary retention; osteoporosis; angina pectoris;

CC   This is the nucleotide sequence of the HGS EST 557082 used in the method
CC   of the invention involving the G-protein coupled receptor, HFGAN72Y. Its
CC   polypeptides and polynucleotides are useful for diagnosing susceptibility
CC   to diseases by detecting mutations in the HFGAN72Y gene using probes
CC   containing the HFGAN72Y nucleotide sequence, and can diagnose diseases
CC   associated with HFGAN72Y imbalance by determining HFGAN72Y polypeptide or
CC   mRNA expression levels. Agonists/antagonists can be used in treatment to
CC   activate/inhibit HFGAN72Y activity, in addition to direct administration
CC   of antisense sequences to prevent expression, or HFGAN72Y polypeptides to
CC   treat conditions associated with a lack HFGAN72Y protein. Gene therapy
CC   may also be used to affect endogenous HFGAN72Y polypeptide production.
CC   HFGAN72Y antibodies are useful for inducing an immune response to
CC   immunise and prevent diseases, and for isolating HFGAN72Y clones or
CC   purifying the polypeptides by affinity chromatography. HFGAN72Y
CC   polypeptides can be administered directly or as a vaccine to inoculate
CC   against diseases. Diseases diagnosed, prevented or treated include HIV-1
CC   or HIV-2 infections, pain, cancers, anorexia, bulimia, asthma,
CC   Parkinson's disease, acute heart failure, hypotension, hypertension,
CC   urinary retention, osteoporosis, angina pectoris, myocardial infarction,
CC   ulcers; allergies, benign prostatic hypertrophy, and psychotic and
CC   neurological disorders. The HFGAN72Y polypeptide is also useful for
CC   mapping the gene to a chromosome, allowing gene inheritance to be studied
CC   through linkage analysis.
XX
SQ   Sequence 1133 BP; 202 A; 366 C; 314 G; 251 T; 0 U; 0 Other;

      Query Match   99.9%;   Score 1131.4; DB 2;   Length 1133;
      Best Local Similarity   99.9%;   Pred. No. 4.5e-263;
      Matches 1132; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```
Db      1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy    121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy    841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Qy    901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy    961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy   1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy   1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG 1133
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG 1133


RESULT 4
ABA96020
ID    ABA96020 standard; cDNA; 1133 BP.
XX
AC    ABA96020;
XX
DT    12-MAR-2002  (first entry)
XX
DE    HGS EST 557082.
XX
KW    G-protein; receptor; HFGAN72Y; cytostatic; cardiant; analgesic; cancer;
KW    nootropic; tranquillising; neuroprotective; anti-asthmatic; gene therapy;
KW    infection; HIV-1; pain; anorexia; bulimia; Parkinson's disease; ulcer;
KW    cardiac disease; urinary retention; asthma; allergy; psychotic disorder;
KW    benign prostatic hypertrophy; neurological disorder; anxiety; delirium;
KW    schizophrenia; manic depression; dementia; mental retardation; EST;
KW    dyskinesia; Huntington's disease; Tourette's syndrome; HIV-2;
KW    HGS EST 557082; expressed sequence tag; ss.
XX
OS    Homo sapiens.
XX
PN    EP1156110-A2.
XX
PD    21-NOV-2001.
XX
PF    27-OCT-1997; 2001EP-00203010.
XX
PR    30-APR-1997;    97US-00846705.
PR    27-OCT-1997;    97EP-00308554.
XX
PA    (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI    Bergsma DJ,  Ellis CE;
XX
DR    WPI; 2002-084320/12.
XX
PT    New polynucleotide encoding a G-protein coupled receptor designated
PT    HFGAN72Y is useful to diagnose and treat associated diseases including
PT    cancer, infection, cardiac disease and psychotic and neurological
```

PT   disorders.
XX
PS   Example 1; Page 18-19; 22pp; English.
XX
CC   The sequence represents HGS EST 557082. The invention relates to a novel
CC   isolated polynucleotide encoding HFGAN72Y polypeptide. The polypeptide of
CC   the invention has cytostatic, cardiant, analgesic, tranquillising,
CC   nootropic, neuroprotective, and anti-asthmatic activity. The HFGAN72Y has
CC   a use in gene therapy. The HFGAN72Y polynucleotide or an HFGAN72Y
CC   polypeptide agonist are used to treat a subject in need of enhanced
CC   HFGAN72Y activity or expression. An HFGAN72Y antagonist or competitor, or
CC   nucleic acid which inhibits HFGAN72Y expression is used to treat a
CC   subject in need of decreased HFGAN72Y activity or expression. HFGAN72Y-
CC   associated diseases include infections, particularly by HIV-1 or HIV-2,
CC   pain, anorexia, bulimia, Parkinson's disease, cardiac diseases, cancers,
CC   ulcers, urinary retention, asthma, allergies, benign prostatic
CC   hypertrophy, and psychotic and neurological disorders including anxiety,
CC   schizophrenia, manic depression, delirium, dementia, severe mental
CC   retardation and dyskinesias such as Huntington's disease and Tourette's
CC   syndrome
XX
SQ   Sequence 1133 BP; 202 A; 366 C; 314 G; 251 T; 0 U; 0 Other;

     Query Match   99.9%;   Score 1131.4; DB 6;   Length 1133;
     Best Local Similarity   99.9%;   Pred. No. 4.5e-263;
     Matches 1132; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ACCAACTACTTCATTGTCAACCTGTCCCTGCCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy   301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy   361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy   421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Db      421  GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG  480

Qy      481  GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481  GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT  540

Qy      541  GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541  GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA  600

Qy      601  GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT  660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601  GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT  660

Qy      661  ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC  720
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661  ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC  720

Qy      721  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC  780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC  780

Qy      781  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC  840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC  840

Qy      841  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG  900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG  900

Qy      901  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT  960

Qy      961  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC  1020

Qy     1021  ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC  1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021  ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC  1080

Qy     1081  CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG  1133
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081  CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG  1133
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RESULT 5
AAV68511
ID   AAV68511 standard; cDNA; 1170 BP.
XX
AC   AAV68511;
XX
DT   29-JAN-1999 (first entry)
XX
DE   Nucleotide sequence of HFGAN72Y a G-protein coupled receptor.
XX

CC   This is the nucleotide sequence of the G-protein coupled receptor,
CC   HFGAN72Y used in the method of the invention. HFGAN72Y polypeptides and
CC   polynucleotides are useful for diagnosing susceptibility to diseases by
CC   detecting mutations in the HFGAN72Y gene using probes containing the
CC   HFGAN72Y nucleotide sequence, and can diagnose diseases associated with
CC   HFGAN72Y imbalance by determining HFGAN72Y polypeptide or mRNA expression
CC   levels. Agonists/antagonists can be used in treatment to activate/inhibit
CC   HFGAN72Y activity, in addition to direct administration of antisense
CC   sequences to prevent expression, or HFGAN72Y polypeptides to treat
CC   conditions associated with a lack HFGAN72Y protein. Gene therapy may also
CC   be used to affect endogenous HFGAN72Y polypeptide production. HFGAN72Y
CC   antibodies are useful for inducing an immune response to immunise and
CC   prevent diseases, and for isolating HFGAN72Y clones or purifying the
CC   polypeptides by affinity chromatography. HFGAN72Y polypeptides can be
CC   administered directly or as a vaccine to inoculate against diseases.
CC   Diseases diagnosed, prevented or treated include HIV-1 or HIV-2
CC   infections, pain, cancers, anorexia, bulimia, asthma, Parkinson's
CC   disease, acute heart failure, hypotension, hypertension, urinary
CC   retention, osteoporosis, angina pectoris, myocardial infarction, ulcers;
CC   allergies, benign prostatic hypertrophy, and psychotic and neurological
CC   disorders. The HFGAN72Y polypeptide is also useful for mapping the gene

```
CC   to a chromosome, allowing gene inheritance to be studied through linkage
CC   analysis
XX
SQ   Sequence 1170 BP; 208 A; 381 C; 322 G; 259 T; 0 U; 0 Other;

    Query Match              99.6%;   Score 1128.2;   DB 2;   Length 1170;
    Best Local Similarity    99.7%;   Pred. No. 2.7e-262;
    Matches 1130;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;


Qy        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
            ||||||||||||||||||||||||||||||||||||||||||Î|||||||||||||||||||||
Db        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||.|||||||
Db      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy      421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy      541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy      601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy      661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCGGGGC 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG 1133
              |||||||||||||||||||||||||||||||| ||||||||| |||||||||||||
Db       1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGCTCTGTCCTGCCCATCGTGCCCCGG 1133


RESULT 6
ABA96019
ID   ABA96019 standard; cDNA; 1170 BP.
XX
AC   ABA96019;
XX
DT   12-MAR-2002   (first entry)
XX
DE   G-protein coupled receptor (HFGAN72Y) cDNA.
XX
KW   G-protein; receptor; HFGAN72Y; cytostatic; cardiant; analgesic; cancer;
KW   nootropic; tranquillising; neuroprotective; anti-asthmatic; gene therapy;
KW   infection; HIV-1; pain; anorexia; bulimia; Parkinson's disease; ulcer;
KW   cardiac disease; urinary retention; asthma; allergy; psychotic disorder;
KW   benign prostatic hypertrophy; neurological disorder; anxiety; delirium;
KW   schizophrenia; manic depression; dementia; mental retardation;
KW   dyskinesia; Huntington's disease; Tourette's syndrome; HIV-2; ss.
XX
OS   Homo sapiens.
XX
FH   Key              Location/Qualifiers
FT   CDS              1. .1170
FT                    /*tag= a
FT                    /product= "HGFAN72Y"
XX
PN   EP1156110-A2.
XX
PD   21-NOV-2001.
```

PT   New polynucleotide encoding a G-protein coupled receptor designated
PT   HFGAN72Y is useful to diagnose and treat associated diseases including
PT   cancer, infection, cardiac disease and psychotic and neurological
PT   disorders.
XX
PS   Claim 3; Page 7; 22pp; English.
XX
CC   The sequence encodes G-protein coupled receptor HFGAN72Y. The invention
CC   relates to a novel isolated polynucleotide encoding HFGAN72Y polypeptide.
CC   The polypeptide of the invention has cytostatic, cardiant, analgesic,
CC   tranquillising, nootropic, neuroprotective, and anti-asthmatic activity.
CC   The HFGAN72Y has a use in gene therapy. The HFGAN72Y polynucleotide or an
CC   HFGAN72Y polypeptide agonist are used to treat a subject in need of
CC   enhanced HFGAN72Y activity or expression. An HFGAN72Y antagonist or
CC   competitor, or nucleic acid which inhibits HFGAN72Y expression is used to
CC   treat a subject in need of decreased HFGAN72Y activity or expression.
CC   HFGAN72Y-associated diseases include infections, particularly by HIV-1 or
CC   HIV-2, pain, anorexia, bulimia, Parkinson's disease, cardiac diseases,
CC   cancers, ulcers, urinary retention, asthma, allergies, benign prostatic
CC   hypertrophy, and psychotic and neurological disorders including anxiety,
CC   schizophrenia, manic depression, delirium, dementia, severe mental
CC   retardation and dyskinesias such as Huntington's disease and Tourette's
CC   syndrome
XX
SQ   Sequence 1170 BP; 208 A; 381 C; 322 G; 259 T; 0 U; 0 Other;

      Query Match   99.6%;   Score 1128.2;   DB 6;   Length 1170;
      Best Local Similarity   99.7%;   Pred. No. 2.7e-262;
      Matches 1130; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

Qy   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Db      181  CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC  240

Qy      241  ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241  ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG  300

Qy      301  CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301  CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG  360

Qy      361  GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361  GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC  420

Qy      421  GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421  GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG  480

Qy      481  GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481  GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT  540

Qy      541  GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541  GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA  600

Qy      601  GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT  660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601  GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT  660

Qy      661  ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661  ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC  720

Qy      721  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC  780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC  780

Qy      781  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC  840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC  840

Qy      841  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG  900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG  900

Qy      901  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT  960

Qy      961  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC  1020

Qy     1021  ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC  1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021  ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC  1080
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Qy      1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG 1133
             ||||||||||||||||||||||||||||| ||||||||| ||||||||||||||
Db      1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGCTCTGTCCTGCCCATCGTGCCCCGG 1133
```

RESULT 7
AAV63468
ID   AAV63468 standard; cDNA; 1564 BP.
XX
AC   AAV63468;
XX
DT   26-JAN-1999 (first entry)
XX
DE   cDNA encoding G-protein coupled receptor (HFGAN72X) polypeptide.
XX
KW   G-protein coupled receptor; HFGAN72X; HIV infection; anorexia; cancer;
KW   bulimia; asthma; Parkinson's disease; acute heart failure;
KW   urinary retention; osteoporosis; angina pectoris; myocardial infarction;
KW   benign prostatic hypertrophy; neurological disorder; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   154. .1431
FT   /*tag= a
FT   /product= "HFGAN72X"
XX
PN   EP875566-A2.
XX
PD   04-NOV-1998.
XX
PF   27-OCT-1997;   97EP-00308563.
XX
PR   30-APR-1997;   97US-00846704.
XX
PA   (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI   Bergsma DJ, Ellis CE;
XX
DR   WPI; 1998-559432/48.
DR   P-PSDB; AAW80456.
XX
PT   New human G-protein coupled receptor HFGAN72X polypeptide and
PT   polynucleotide - useful as diagnostic reagents and for treating e.g. HIV
PT   infection, cancer and Parkinson's disease.
XX
PS   Claim 3; Page 7; 24pp; English.
XX
CC   The present sequence encodes a G-protein coupled receptor (HFGAN72X)
CC   polypeptide. HFGAN72X polypeptides and polynucleotides are useful for
CC   diagnosing diseases related to over or under expression of HFGAN72X
CC   proteins by identifying mutations in the HFGAN72X gene using HFGAN72X
CC   probes, or determining HFGAN72X protein or mRNA expression levels.
CC   HFGAN72X polypeptides are also useful for screening for compounds which
CC   affect activity of the protein. Diseases that can be treated with
CC   HFGAN72X include HIV infections, pain, anorexia, cancers, bulimia,

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CC   asthma, Parkinson's disease, acute heart failure, hypotension,
CC   hypertension, urinary retention, osteoporosis, angina pectoris,
CC   myocardial infarction, ulcers, allergies, benign prostatic hypertrophy,
CC   and psychotic and neurological disorders
XX
SQ   Sequence 1564 BP; 271 A; 511 C; 435 G; 347 T; 0 U; 0 Other;

     Query Match            95.9%;  Score 1086.4;  DB 2;  Length 1564;
     Best Local Similarity  99.9%;  Pred. No. 3.6e-252;
     Matches 1087;  Conservative   0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy        61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy       121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy       181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy       241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy       301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy       361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy       421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy       481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy       541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy       601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy       661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081 CTCAGTGG 1088
              ||||||||
Db       1234 CTCAGTGG 1241


RESULT 8
AAV68514
ID    AAV68514 standard; cDNA; 1564 BP.
XX
AC    AAV68514;
XX
DT    29-JAN-1999  (first entry)
XX
DE    Nucleotide sequence of a probe HGS EST 554692.
XX
KW    Probe HGS EST 554692; G-protein coupled receptor family; HFGAN72Y;
KW    mutation; probe; agonist; antagonist; activation; inhibition;
KW    gene therapy; antibody; immune response; vaccine; HIV-1; HIV-2; cancer;
KW    anorexia; bulimia; asthma; Parkinson's disease; acute heart failure;
KW    hypotension; hypertension; urinary retention; osteoporosis;
KW    angina pectoris; myocardial infarction; ulcer; allergies;
KW    psychotic disorder; neurological disorder; gene mapping; ss.
XX
OS    Synthetic.
OS    Homo sapiens.
XX
PN    EP875565-A2.
XX
PD    04-NOV-1998.
XX
PF    27-OCT-1997;   97EP-00308554.
```

PT   New G-protein coupled receptor HFGAN72Y polypeptide and polynucleotide -
PT   useful as diagnostic reagents and for prevention and treatment of HIV
PT   infections, cancer, osteoporosis and Parkinson's disease.
XX
PS   Example 1; Page 19-20; 22pp; English.
XX
CC   This is the nucleotide sequence of the probe HGS EST 554692 used in the
CC   method of the invention involving the G-protein coupled receptor,
CC   HFGAN72Y. Its polypeptides and polynucleotides are useful for diagnosing
CC   susceptibility to diseases by detecting mutations in the HFGAN72Y gene
CC   using probes containing the HFGAN72Y nucleotide sequence, and can
CC   diagnose diseases associated with HFGAN72Y imbalance by determining
CC   HFGAN72Y polypeptide or mRNA expression levels. Agonists/antagonists can
CC   be used in treatment to activate/inhibit HFGAN72Y activity, in addition
CC   to direct administration of antisense sequences to prevent expression, or
CC   HFGAN72Y polypeptides to treat conditions associated with a lack HFGAN72Y
CC   protein. Gene therapy may also be used to affect endogenous HFGAN72Y
CC   polypeptide production. HFGAN72Y antibodies are useful for inducing an
CC   immune response to immunise and prevent diseases, and for isolating
CC   HFGAN72Y clones or purifying the polypeptides by affinity chromatography.
CC   HFGAN72Y polypeptides can be administered directly or as a vaccine to
CC   inoculate against diseases. Diseases diagnosed, prevented or treated
CC   include HIV-1 or HIV-2 infections, pain, cancers, anorexia, bulimia,
CC   asthma, Parkinson's disease, acute heart failure, hypotension,
CC   hypertension, urinary retention, osteoporosis, angina pectoris,
CC   myocardial infarction, ulcers; allergies, benign prostatic hypertrophy,
CC   and psychotic and neurological disorders. The HFGAN72Y polypeptide is
CC   also useful for mapping the gene to a chromosome, allowing gene
CC   inheritance to be studied through linkage analysis
XX
SQ   Sequence 1564 BP; 269 A; 508 C; 436 G; 347 T; 0 U; 4 Other;

     Query Match   95.9%;   Score 1086.4; DB 2; Length 1564;
     Best Local Similarity   99.9%;   Pred. No. 3.6e-252;
     Matches 1087; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

```
Qy      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy      421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy      541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy      601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy      661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy      721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy      781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1174  ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy     1081  CTCAGTGG 1088
             ||||||||
Db     1234  CTCAGTGG 1241
```

RESULT 9
AAF32103
ID   AAF32103 standard; cDNA; 1564 BP.
XX
AC   AAF32103;
XX
DT   10-APR-2001   (first entry)
XX
DE   Human HFGAN72 receptor coding sequence SEQ ID NO: 12.
XX
KW   Human; mouse; rat; Lig72A; Lig72B; neuropeptide receptor; HFGAN72;
KW   truncation mutant; ligand; neurodegenerative disorder; pain;
KW   eating disorder; behaviour disorder; mood disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200100787-A2.
XX
PD   04-JAN-2001.
XX
PF   22-JUN-2000; 2000WO-US017251.
XX
PR   25-JUN-1999;   99US-0141156P.
XX
PA   (SMIK) SMITHKLINE BEECHAM CORP.
PA   (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI   Bingham S, Darker J, Liu W, Martin JD, Parsons AA, Patel SR;
XX
DR   WPI; 2001-071483/08.
XX
PT   Polynucleotides encoding Lig 72A polypeptides or their variants, which
PT   are useful in the treatment of a disease or disorder associated with
PT   pain, e.g. enhanced or exaggerated sensitivity to pain, hyperalgesia,
PT   neuropathic pain and back pain.
XX
PS   Disclosure; Fig 6; 101pp; English.
XX
CC   The present invention provides the protein and coding sequences for the
CC   human, mouse and rat HFGAN receptor ligand Lig72A. It also provides
CC   truncated mutant versions. These, and their agonists and antagonists, are
CC   all useful in the treatment of eating, neurodegenerative, behaviour,
CC   mood, sexual, hormonal and sleep disorders, pain, depression, epilepsy
CC   and acute inflammatory conditions
XX
SQ   Sequence 1564 BP; 271 A; 511 C; 435 G; 347 T; 0 U; 0 Other;

      Query Match   95.9%; Score 1086.4; DB 4; Length 1564;
      Best Local Similarity   99.9%; Pred. No. 3.6e-252;
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Matches 1087; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

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Qy      1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy    121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993
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Qy        841  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG  900
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy        901  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT  960
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1054  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy        961  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021  ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174  ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081  CTCAGTGG 1088
               ||||||||
Db       1234  CTCAGTGG 1241
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RESULT 10
ABA96021
ID   ABA96021 standard; cDNA; 1564 BP.
XX
AC   ABA96021;
XX
DT   12-MAR-2002   (first entry)
XX
DE   HGS EST 554692.
XX
KW   G-protein; receptor; HFGAN72Y; cytostatic; cardiant; analgesic; cancer;
KW   nootropic; tranquillising; neuroprotective; anti-asthmatic; gene therapy;
KW   infection; HIV-1; pain; anorexia; bulimia; Parkinson's disease; ulcer;
KW   cardiac disease; urinary retention; asthma; allergy; psychotic disorder;
KW   benign prostatic hypertrophy; neurological disorder; anxiety; delirium;
KW   schizophrenia; manic depression; dementia; mental retardation; EST;
KW   dyskinesia; Huntington's disease; Tourette's syndrome; HIV-2;
KW   HGS EST 554692; expressed sequence tag; probe; ss.
XX
OS   Homo sapiens.
XX
PN   EP1156110-A2.
XX
PD   21-NOV-2001.
XX
PF   27-OCT-1997; 2001EP-00203010.
XX
PR   30-APR-1997;   97US-00846705.
PR   27-OCT-1997;   97EP-00308554.
XX
PA   (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI   Bergsma DJ, Ellis CE;
XX
DR   WPI; 2002-084320/12.

XX
PT New polynucleotide encoding a G-protein coupled receptor designated
PT HFGAN72Y is useful to diagnose and treat associated diseases including
PT cancer, infection, cardiac disease and psychotic and neurological
PT disorders.
XX
PS Example 1; Page 19-20; 22pp; English.
XX
CC The sequence represents HGS EST 554692. The sequence was used in the
CC invention as a probe to screen a human genomic placenta phage library.
CC The invention relates to a novel isolated polynucleotide encoding
CC HFGAN72Y polypeptide. The polypeptide of the invention has cytostatic,
CC cardiant, analgesic, tranquillising, nootropic, neuroprotective, and anti
CC -asthmatic activity. The HFGAN72Y has a use in gene therapy. The HFGAN72Y
CC polynucleotide or an HFGAN72Y polypeptide agonist are used to treat a
CC subject in need of enhanced HFGAN72Y activity or expression. An HFGAN72Y
CC antagonist or competitor, or nucleic acid which inhibits HFGAN72Y
CC expression is used to treat a subject in need of decreased HFGAN72Y
CC activity or expression. HFGAN72Y-associated diseases include infections,
CC particularly by HIV-1 or HIV-2, pain, anorexia, bulimia, Parkinson's
CC disease, cardiac diseases, cancers, ulcers, urinary retention, asthma,
CC allergies, benign prostatic hypertrophy, and psychotic and neurological
CC disorders including anxiety, schizophrenia, manic depression, delirium,
CC dementia, severe mental retardation and dyskinesias such as Huntington's
CC disease and Tourette's syndrome
XX
SQ Sequence 1564 BP; 269 A; 508 C; 436 G; 347 T; 0 U; 4 Other;

```
     Query Match              95.9%;  Score 1086.4;  DB 6;   Length 1564;
     Best Local Similarity    99.9%;  Pred. No. 3.6e-252;
     Matches 1087;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;


Qy           1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213


Qy          61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273


Qy         121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333


Qy         181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393


Qy         241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453


Qy         301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513


Qy         361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy       421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy       481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy       541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy       601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy       661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy       721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy       781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy       841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy       901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy       961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy      1081 CTCAGTGG 1088
                  ||||||||
Db      1234 CTCAGTGG 1241


RESULT 11
AAI64173
ID   AAI64173 standard; cDNA; 1564 BP.
XX
AC   AAI64173;
```

CC   HFGAN72X polynucleotides (PNs) are used to express HFGAN72X in vivo, to
CC   treat diseases requiring increased activity or expression of HFGAN72X;
CC   for recombinant production of HFGAN72X; diagnose diseases by detecting
CC   mutations in genomic sequences and in chromosome identification and
CC   mapping. HFGAN72X polypeptides are used to raise specific antibodies; as
CC   therapeutic agents; to identify HFGAN72X protein-expressing clones; to
CC   purify HFGAN72X proteins; in vaccines. Cells transformed with HFGAN72X
CC   PNs are used to identify (ant)agonists of HFGAN72X, useful
CC   therapeutically. Nucleic acids that inhibit expression of HFGAN72X and
CC   polypeptides that compete with ligands for binding to HFGAN72X proteins
CC   are also useful therapeutically and diagnostically. HFGAN72X-related
CC   diseases include infections (bacterial, viral, fungal or protozoal,
CC   particularly HIV-1 or -2); pain; cancer; anorexia; bulimia; Parkinson's
CC   disease; acute heart failure; hypotension; hypertension; urinary
CC   retention; osteoporosis; angina pectoris; myocardial infarction; ulcers;
CC   asthma; allergy; benign prostatic hypertrophy; anxiety; schizophrenia;
CC   manic depression; delirium; dementia; severe mental retardation and
CC   dyskinesias
XX
SQ   Sequence 1564 BP; 269 A; 508 C; 436 G; 347 T; 0 U; 4 Other;

      Query Match   95.9%;   Score 1086.4;   DB 6;   Length 1564;
      Best Local Similarity   99.9%;   Pred. No. 3.6e-252;
      Matches 1087; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy   301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy   361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy   421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

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Qy      481  GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      634  GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT  693

Qy      541  GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      694  GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA  753

Qy      601  GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT  660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      754  GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT  813

Qy      661  ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      814  ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC  873

Qy      721  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC  780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      874  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC  933

Qy      781  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC  840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      934  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC  993

Qy      841  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG  900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      994  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG  1053

Qy      901  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT  1113

Qy      961  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC  1173

Qy      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC  1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC  1233

Qy      1081 CTCAGTGG  1088
             ||||||||
Db      1234 CTCAGTGG  1241
```

RESULT 12
AAI64172
ID   AAI64172 standard; cDNA; 1564 BP.
XX
AC   AAI64172;
XX
DT   22-JAN-2002   (first entry)
XX
DE   Human HFGAN72X G coupled receptor polypeptide cDNA.
XX
KW   Antibacterial; fungicide; virucide; protozoacide; anti-HIV; analgesic;
KW   cytostatic; nootropic; antiparkinsonian; cardiant; antiulcer;

CC   The present sequence is that of a cDNA encoding a HFGAN72X polypeptide
CC   (AAG78345). The specification describes a newly isolated polynucleotide
CC   encoding a HFGAN72X G coupled receptor polypeptide. The protein of the
CC   invention has antibacterial, fungicide, virucide, protozoacide, anti-HIV,
CC   cardiant, analgesic, cytostatic, nootropic, antiparkinsonian, antiulcer,
CC   antiasthmatic, tranquiliser, neuroleptic, antidepressant, anticonvulsant
CC   and osteopathic activities. HFGAN72X polynucleotides (PNs) are used to
CC   express HFGAN72X in vivo, to treat diseases requiring increased activity
CC   or expression of HFGAN72X; for recombinant production of HFGAN72X;
CC   diagnose diseases (or susceptibility to them) by detecting mutations in
CC   genomic sequences and in chromosome identification and mapping. HFGAN72X
CC   polypeptides are used to raise specific antibodies; as therapeutic agents
CC   ; to identify HFGAN72X protein-expressing clones; to purify HFGAN72X
CC   proteins; in vaccines. Cells transformed with HFGAN72X PNs are used to
CC   identify (ant)agonists of HFGAN72X, useful therapeutically. Nucleic acids
CC   that inhibit expression of HFGAN72X and polypeptides that compete with
CC   ligands for binding to HFGAN72X proteins are also useful therapeutically
CC   and diagnostically. HFGAN72X-related diseases include infections
CC   (bacterial, viral, fungal or protozoal, particularly HIV-1 or -2); pain;

```
     Query Match              95.9%;   Score 1086.4;  DB 6;   Length 1564;
     Best Local Similarity    99.9%;   Pred. No. 3.6e-252;
     Matches 1087;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy      421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy      541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy      601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy      661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCGGGGC 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCGGGGC 993

Qy    841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy    901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy    961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy   1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy   1081 CTCAGTGG 1088
          ||||||||
Db   1234 CTCAGTGG 1241


RESULT 13
ABZ42789
ID   ABZ42789 standard; DNA; 1564 BP.
XX
AC   ABZ42789;
XX
DT   04-MAR-2003  (first entry)
XX
DE   Human orexin receptor 1 nucleotide SEQ ID NO:367.
XX
KW   G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW   G protein-coupled receptor modulator; antibody; immune-related disease;
KW   growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW   immunological-related cell proliferative disease; autoimmune disease;
KW   Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW   osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW   graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW   psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW   mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW   hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW   ulcer; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200261087-A2.
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PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.
XX
PS Disclosure; Fig 1; 523pp; English.
XX
CC The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention
XX
SQ Sequence 1564 BP; 268 A; 513 C; 436 G; 347 T; 0 U; 0 Other;

    Query Match   95.9%; Score 1086.4; DB 7; Length 1564;
    Best Local Similarity 99.9%; Pred. No. 3.6e-252;
    Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

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Qy    61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
         | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
         | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
         | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
         | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy   301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
         | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy   361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
         | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy   421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
         | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy   481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
         | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy   541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
         | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy   601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
         | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy   661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
         | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy   721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
         | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy   781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
         | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy   841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
         | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy   901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1054  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy       961  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1114  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy      1021  ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1174  ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy      1081  CTCAGTGG 1088
              ||||||||
Db      1234  CTCAGTGG 1241
```

RESULT 14
AAT42827
ID   AAT42827 standard; cDNA; 1110 BP.
XX
AC   AAT42827;
XX
DT   22-FEB-1997   (first entry)
XX
DE   Neuropeptide receptor splice variant-1 gene.
XX
KW   Human; neuropeptide receptor; splice variant; drug screening;
KW   receptor-agonist; receptor-antagonist; anorectic; antitumour;
KW   anticholesterolemic; neuroprotective; anticonvulsant; hypotensive;
KW   sedative; diagnostic; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO9634877-A1.
XX
PD   07-NOV-1996.
XX
PF   05-MAY-1995;   95WO-US005616.
XX
PR   05-MAY-1995;   95WO-US005616.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Soppet DR, Li Y, Rosen CA;
XX
DR   WPI; 1996-506094/50.
DR   P-PSDB; AAW06125.
XX
PT   Human neuro-peptide receptor polypeptide(s) - used to identify
PT   antagonists and agonists to such polypeptide(s), e.g. in the treatment of
PT   obesity, Alzheimer's disease, epilepsy, etc.
XX
PS   Disclosure; Page 50-51; 77pp; English.
XX
CC   The sequence encodes human neuropeptide receptor splice variant-1, which
CC   retains activity corresponding to the mature receptor (encoded by
CC   AAT42826). The receptor gene has been isolated from from a human adult
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CC     hypothalamus cDNA library, and is structurally related to the G-protein-
CC     coupled receptor family. The receptor may be used in a drug screening
CC     assay for isolation of receptor-agonists and -antagonists, which may be
CC     used as anorectic, antitumour, anticholesterolemic, neuroprotective,
CC     anticonvulsant, hypotensive or sedative drugs, etc. The DNA may also be
CC     used in genetic disease diagnosis or gene therapy. The receptor and its
CC     corresponding antibody may also be used in therapy and diagnosis
XX
SQ     Sequence 1110 BP; 194 A; 364 C; 305 G; 247 T; 0 U; 0 Other;

     Query Match               95.7%;   Score 1084.8;   DB 2;   Length 1110;
     Best Local Similarity     99.8%;   Pred. No. 7.9e-252;
     Matches 1086;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;


Qy           1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy          61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy         121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy         181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy         241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy         301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy         361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy         421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy         481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy         541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy         601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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```
Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
              |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
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Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1081 CTCAGTGG 1088
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Db       1081 CTCAGTGG 1088
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RESULT 15
AAS00491
ID   AAS00491 standard; cDNA; 1278 BP.
XX
AC   AAS00491;
XX
DT   17-MAY-2001 (first entry)
XX
DE   Human neuropeptide receptor cDNA.
XX
KW   Human; neuropeptide receptor; neuropeptide Y receptor; obesity;
KW   nervous system disorder; hyperproliferative disorder; diabetes mellitus;
KW   cardiovascular disorder; autoimmune disorder; infectious disorder;
KW   eating behaviour disorder; narcolepsy; neurological disease;
KW   narcotics addiction; nicotine addiction; alcohol addiction; gene therapy;
KW   protein co-ordinate data; chromosome 1; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   1. .1278
FT   /*tag= a
FT   /product= "neuropeptide receptor"

PT   A new nucleic acid encoding a human neuropeptide receptor polypeptide,
PT   useful for preventing, treating or ameliorating obesity, narcolepsy,
PT   neurological disease and addiction to narcotics, nicotine and alcohol.

XX

PS   Claim 4; Fig 1; 385pp; English.

XX

CC   The present sequence encodes for a novel human neuropeptide receptor
CC   which shows sequence homology to the neuropeptide Y receptor. Two splice
CC   variants of the neuropeptide receptor (AAU00439-AAU00440) and a possible
CC   mutant (AAU00442) are also described. Polypeptides and polynucleotides of
CC   the neuropeptide receptor are useful for diagnosing, preventing, or
CC   treating a pathological condition in a subject related to the central
CC   nervous and peripheral nervous systems (CNS and PNS). The polypeptides
CC   and polynucleotides may be used to treat hyperproliferative,
CC   cardiovascular, autoimmune, nervous system or infectious disorders e.g.
CC   cancer, heart disease, rheumatoid arthritis, Alzheimer's disease, HIV
CC   infection and diabetes mellitus. In particular they are useful for
CC   preventing, treating or ameliorating a medical condition in a mammal such
CC   as obesity/eating behaviour disorders, narcolepsy, neurological disease,
CC   addiction to narcotics, nicotine and alcohol, chronic pain, acute pain,
CC   migraine headaches and anxiety disorders. The polynucleotides encoding
CC   the neuropeptide receptor can also be used in gene therapy methods for
CC   treating such diseases

XX

SQ   Sequence 1278 BP; 220 A; 426 C; 347 G; 285 T; 0 U; 0 Other;

    Query Match   95.7%;   Score 1084.8; DB 4;   Length 1278;
    Best Local Similarity   99.8%;   Pred. No. 8.2e-252;
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840

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Db    841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy    901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
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Db      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy      1081 CTCAGTGG 1088
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OM nucleic - nucleic search, using sw model

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Perfect score: 1133
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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                  SUMMARIES

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1	1131.4	99.9	1133	2	US-08-846-705-3	Sequence 3, Appli
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3	1128.2	99.6	1170	2	US-08-846-705-1	Sequence 1, Appli
4	1114.4	98.4	1116	4	US-08-462-509B-5	Sequence 5, Appli
5	1086.4	95.9	1209	4	US-08-462-509B-1	Sequence 1, Appli
6	1086.4	95.9	1564	2	US-08-846-705-4	Sequence 4, Appli
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8	1086.4	95.9	1564	3	US-08-846-704-3	Sequence 3, Appli
9	1084.8	95.7	1110	4	US-08-462-509B-3	Sequence 3, Appli
10	1081.6	95.5	1209	5	PCT-US95-05616-1	Sequence 1, Appli

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11   1076.8   95.0    1110   5   PCT-US95-05616-3      Sequence 3, Appli
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13    670.6   59.2     789   3   US-08-513-974B-55     Sequence 55, Appl
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16    249.2   22.0    9785   4   US-09-479-128-1       Sequence 1, Appli
17    163.2   14.4    1293   3   US-09-255-368-7       Sequence 7, Appli
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ALIGNMENTS

RESULT 1
US-08-846-705-3
; Sequence 3, Application US/08846705
; Patent No. 5935814
;   GENERAL INFORMATION:
;   APPLICANT: BERGSMA, DERK J.
;   APPLICANT: ELLIS, CATHERINE E
;   TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED
;   NUMBER OF SEQUENCES: 5
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: RATNER & PRESTIA
;   STREET: P.O. BOX 980
;   CITY: VALLEY FORGE
;   STATE: PA
;   COUNTRY: USA
;   ZIP: 19482
;   COMPUTER READABLE FORM:

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   Query Match              99.9%;  Score 1131.4;  DB 2;  Length 1133;
   Best Local Similarity    99.9%;  Pred. No. 9.6e-261;
   Matches 1132; Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy        61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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;   GENERAL INFORMATION:
;     APPLICANT:  LI, ET AL.
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Qy       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy      421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy      541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy      601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy      661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy      721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy      781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy     1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG 1133
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Db     1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG 1133
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RESULT 3
US-08-846-705-1
; Sequence 1, Application US/08846705
; Patent No. 5935814
; GENERAL INFORMATION:
;   APPLICANT: BERGSMA, DERK J.
;   APPLICANT: ELLIS, CATHERINE E
;   TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED
;   NUMBER OF SEQUENCES: 5
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: RATNER & PRESTIA
;   STREET: P.O. BOX 980
;   CITY: VALLEY FORGE
;   STATE: PA
;   COUNTRY: USA
;   ZIP: 19482
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/846,705
;   FILING DATE: 30-APR-1997
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: PRESTIA, PAUL F
;   REGISTRATION NUMBER: 23,031
;   REFERENCE/DOCKET NUMBER: GH-70003
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 610-407-0700
;   TELEFAX: 610-407-0701
;   TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1170 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
US-08-846-705-1

   Query Match   99.6%; Score 1128.2; DB 2; Length 1170;
   Best Local Similarity   99.7%; Pred. No. 5.6e-260;
   Matches 1130; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

Qy   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db    61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy   301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy   361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy   421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db   421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy   481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy   541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy   601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db   601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy   661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy   721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy   781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy   841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy   901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
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Qy      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy     1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG 1133
            |||||||||||||||||||||||||||||| ||||||||| ||||||||||||
Db     1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGCTCTGTCCTGCCCATCGTGCCCCGG 1133
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RESULT 4
US-08-462-509B-5
; Sequence 5, Application US/08462509B
; Patent No. 6410701
;   GENERAL INFORMATION:
;   APPLICANT: Soppet, Daniel et al
;   TITLE OF INVENTION: Human Neuropeptide Receptor
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Human Genome Sciences, Inc.
;   STREET: 9410 Key West Avenue
;   CITY: Rockiville
;   STATE: MD
;   COUNTRY: USA
;   ZIP: 20850
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/462,509B
;   FILING DATE: 05-JUN-1995
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: WO PCT/US95/05616
;   FILING DATE: 05-MAY-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Wales, Michele M.
;   REGISTRATION NUMBER: 43,975
;   REFERENCE/DOCKET NUMBER: PF168P1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 301-309-8504
;   TELEFAX: 301-309-8439
;   INFORMATION FOR SEQ ID NO: 5:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1116 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   FEATURE:
;   NAME/KEY: CDS
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Query Match   98.4%;   Score 1114.4;   DB 4;   Length 1116;
Best Local Similarity   99.9%;   Pred. No. 1.1e-256;
Matches 1115;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

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Qy      1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
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Db      1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGACCCC 60

Qy     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy    121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCC 1116
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Db       1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCC 1116
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RESULT 5
US-08-462-509B-1
; Sequence 1, Application US/08462509B
; Patent No. 6410701
;   GENERAL INFORMATION:
;   APPLICANT: Soppet, Daniel et al
;   TITLE OF INVENTION: Human Neuropeptide Receptor
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Human Genome Sciences, Inc.
;   STREET: 9410 Key West Avenue
;   CITY: Rockiville
;   STATE: MD
;   COUNTRY: USA
;   ZIP: 20850
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/462,509B
;   FILING DATE: 05-JUN-1995
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: WO PCT/US95/05616
;   FILING DATE: 05-MAY-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Wales, Michele M.
;   REGISTRATION NUMBER: 43,975

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   Query Match                95.9%;   Score 1086.4;   DB 4;   Length 1209;
   Best Local Similarity      99.9%;   Pred. No. 5.2e-250;
   Matches 1087;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;


Qy         1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60


Qy        61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
             ||||||||||||||||||||||||||||||||||||||||||·||||||||||||||||||
Db        61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120


Qy       121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180


Qy       181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db       181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240


Qy       241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300


Qy       301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360


Qy       361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Db       361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420


Qy       421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db       421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480


Qy       481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Db       481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540


Qy       541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy    841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy    901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy    961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy   1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy   1081 CTCAGTGG 1088
          ||||||||
Db   1081 CTCAGTGG 1088
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RESULT 6
US-08-846-705-4
; Sequence 4, Application US/08846705
; Patent No. 5935814
;   GENERAL INFORMATION:
;   APPLICANT: BERGSMA, DERK J.
;   APPLICANT: ELLIS, CATHERINE E
;   TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED
;   NUMBER OF SEQUENCES: 5
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: RATNER & PRESTIA
;   STREET: P.O. BOX 980
;   CITY: VALLEY FORGE
;   STATE: PA
;   COUNTRY: USA
;   ZIP: 19482
;   COMPUTER READABLE FORM:

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    Query Match              95.9%;   Score 1086.4;  DB 2;   Length 1564;
    Best Local Similarity    99.9%;   Pred. No. 5.6e-250;
    Matches 1087;  Conservative     0;  Mismatches     1;  Indels    0;  Gaps    0;


Qy         1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213


Qy        61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273


Qy       121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333


Qy       181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
             ||||i|||||||||||||||||||||||||||||||||||||||||||||||||||i||||
Db       334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393


Qy       241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453


Qy       301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513


Qy       361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      514  GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC  573

Qy      421  GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG  480
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      574  GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG  633

Qy      481  GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT  540
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      634  GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT  693

Qy      541  GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA  600
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      694  GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA  753

Qy      601  GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT  660
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      754  GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT  813

Qy      661  ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC  720
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      814  ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC  873

Qy      721  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC  780
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      874  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC  933

Qy      781  CCCTCAGACCAGCTGGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC  840
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      934  CCCTCAGACCAGCTGGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC  993

Qy      841  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG  900
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      994  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG  1053

Qy      901  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT  960
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT  1113

Qy      961  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC  1020
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC  1173

Qy      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC  1080
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC  1233

Qy      1081 CTCAGTGG  1088
                  ||||||||
Db      1234 CTCAGTGG  1241
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RESULT 7
US-08-846-704-1
; Sequence 1, Application US/08846704
; Patent No. 6020157
;   GENERAL INFORMATION:

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   Query Match              95.9%;   Score 1086.4;  DB 3;   Length 1564;
   Best Local Similarity    99.9%;   Pred. No. 5.6e-250;
   Matches 1087;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;


Qy         1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
             ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db       154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213


Qy        61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273


Qy       121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333


Qy       181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      334   CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy      241   ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      394   ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy      301   CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      454   CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy      361   GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      514   GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy      421   GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      574   GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy      481   GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      634   GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy      541   GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      694   GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy      601   GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      754   GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy      661   ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      814   ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy      721   AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      874   AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy      781   CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      934   CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy      841   CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      994   CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy      901   ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1054  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy      961   AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1114  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy      1021  ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy   1081 CTCAGTGG 1088
               | | | | | | | |
Db   1234 CTCAGTGG 1241

RESULT 8
US-08-846-704-3
; Sequence 3, Application US/08846704
; Patent No. 6020157
;   GENERAL INFORMATION:
;   APPLICANT: BERGSMA, DERK J.
;   APPLICANT: ELLIS, CATHERINE E.
;   TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED
;   NUMBER OF SEQUENCES: 4
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: RATNER & PRESTIA
;   STREET: P.O. BOX 980
;   CITY: VALLEY FORGE
;   STATE: PA
;   COUNTRY: USA
;   ZIP: 19482
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/846,704
;   FILING DATE: 30-APR-1997
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: PRESTIA, PAUL F
;   REGISTRATION NUMBER: 23,031
;   REFERENCE/DOCKET NUMBER: GH-70002
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 610-407-0700
;   TELEFAX: 610-407-0701
;   TELEX: 846169
;   INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1564 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
US-08-846-704-3

   Query Match   95.9%; Score 1086.4; DB 3; Length 1564;
   Best Local Similarity 99.9%; Pred. No. 5.6e-250;
   Matches 1087; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60

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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy     121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy     181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy     241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy     301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy     361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy     421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy     481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy     541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy     601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy     661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     314 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy     721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy     781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy     841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy     1081 CTCAGTGG 1088
            ||||||||
Db     1234 CTCAGTGG 1241


RESULT 9
US-08-462-509B-3
; Sequence 3, Application US/08462509B
; Patent No. 6410701
;   GENERAL INFORMATION:
;     APPLICANT:  Soppet, Daniel et al
;     TITLE OF INVENTION:  Human Neuropeptide Receptor
;     NUMBER OF SEQUENCES:  12
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Human Genome Sciences, Inc.
;       STREET:  9410 Key West Avenue
;       CITY:  Rockiville
;       STATE:  MD
;       COUNTRY:  USA
;       ZIP:  20850
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/462,509B
;       FILING DATE:  05-JUN-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  WO PCT/US95/05616
;       FILING DATE:  05-MAY-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Wales, Michele M.
;       REGISTRATION NUMBER:  43,975
;       REFERENCE/DOCKET NUMBER:  PF168P1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  301-309-8504
;       TELEFAX:  301-309-8439
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1110 base pairs
;       TYPE:  nucleic acid
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   Query Match            95.7%;   Score 1084.8;   DB 4;   Length 1110;
   Best Local Similarity  99.8%;   Pred. No. 1.2e-249;
   Matches 1086;  Conservative     0;  Mismatches    2;  Indels    0;  Gaps    0;


Qy        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60


Qy       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120


Qy      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180


Qy      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240


Qy      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300


Qy      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360


Qy      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420


Qy      421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480


Qy      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540


Qy      541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600


Qy      601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660


Qy      661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661   ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy      721   AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721   AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy      781   CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781   CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy      841   CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841   CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy      901   ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
              |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db      901   ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960

Qy      961   AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961   AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy     1021   ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021   ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy     1081   CTCAGTGG 1088
              ||||||||
Db     1081   CTCAGTGG 1088
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RESULT 10
PCT-US95-05616-1
; Sequence 1, Application PC/TUS9505616
;   GENERAL INFORMATION:
;   APPLICANT: LI, ET AL.
;   TITLE OF INVENTION: Human Neuropeptide Receptor
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
;   ADDRESSEE: CECCHI, STEWART & OLSTEIN
;   STREET: 6 BECKER FARM ROAD
;   CITY: ROSELAND
;   STATE: NEW JERSEY
;   COUNTRY: USA
;   ZIP: 07068
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 INCH DISKETTE
;   COMPUTER: IBM PS/2
;   OPERATING SYSTEM: MS-DOS
;   SOFTWARE: WORD PERFECT 5.1
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US95/05616
;   FILING DATE: concurrently
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:

;   NAME: FERRARO, GREGORY D.
;   REGISTRATION NUMBER: 36,134
;   REFERENCE/DOCKET NUMBER: 325800-268
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 201-994-1700
;   TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1209 BASE PAIRS
;   TYPE: NUCLEIC ACID
;   STRANDEDNESS: SINGLE
;   TOPOLOGY: LINEAR
;   MOLECULE TYPE: cDNA
PCT-US95-05616-1

  Query Match   95.5%;   Score 1081.6; DB 5;   Length 1209;
  Best Local Similarity   99.6%;   Pred. No. 7.3e-249;
  Matches 1084; Conservative   0; Mismatches   4; Indels   0; Gaps   0;

Qy   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
            ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   121 TACCCAAAACAGTATGAGTGGGTCCTCATCCCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy   301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy.   361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy   421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy   481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy   541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Db       541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy       601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
             ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 GTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy       661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy       721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
             ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 AACCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy       781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy       841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy       901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy       961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy      1081 CTCAGTGG 1088
             ||||||||
Db      1081 CTCAGTGG 1088


RESULT 11
PCT-US95-05616-3
; Sequence 3, Application PC/TUS9505616
;   GENERAL INFORMATION:
;     APPLICANT:  LI, ET AL.
;     TITLE OF INVENTION:  Human Neuropeptide Receptor
;     NUMBER OF SEQUENCES:  12
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;       ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;       STREET:  6 BECKER FARM ROAD
;       CITY:  ROSELAND
;       STATE:  NEW JERSEY
;       COUNTRY:  USA
;       ZIP:  07068
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  3.5 INCH DISKETTE
;       COMPUTER:  IBM PS/2
```

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   Query Match          95.0%;   Score 1076.8;   DB 5;   Length 1110;
   Best Local Similarity  99.4%;   Pred. No. 1e-247;
   Matches 1081;   Conservative    0;   Mismatches    7;   Indels    0;   Gaps    0;


Qy        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60


Qy       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120


Qy      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180


Qy      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240


Qy      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300


Qy      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360


Qy      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420


Qy      421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Qy    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
          ||||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy    841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy    901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
          ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db    901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960

Qy    961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy   1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy   1081 CTCAGTGG 1088
          ||||||||
Db   1081 CTCAGTGG 1088
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RESULT 12
US-08-513-974B-375
; Sequence 375, Application US/08513974B
; Patent No. 6114139
;   GENERAL INFORMATION:
;   APPLICANT: Hinuma, Shuji
;   APPLICANT: Hosoya, Masaki
;   APPLICANT: Fujii, Ryo
;   APPLICANT: Ohtaki, Tetsuya
;   APPLICANT: Fukusumi, Shoji
;   APPLICANT: Ohgi, Kazuhiro

```
;   TITLE OF INVENTION:  G PROTEIN COUPLED RECEPTOR PROTEIN,
;   TITLE OF INVENTION:  PRODUCTION, AND USE THEREOF
;   NUMBER OF SEQUENCES:  380
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;     STREET:  130 Water Street
;     CITY:  Boston
;     STATE:  MA
;     COUNTRY:  USA
;     ZIP:  02109
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/513,974B
;     FILING DATE:  14-SEP-1995
;     CLASSIFICATION:  536
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  PCT/JP95/01599
;     FILING DATE:  10-AUG-1995
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  JP 7-093989
;     FILING DATE:  19-AUG-1995
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  JP 7-057186
;     FILING DATE:  16-MAR-1995
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  JP 7-007177
;     FILING DATE:  20-JAN-1995
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  JP 6-326611
;     FILING DATE:  28-DEC-1994
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  JP 6-270017
;     FILING DATE:  02-NOV-1994
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  JP 6-236357
;     FILING DATE:  30-SEP-1994
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  JP 6-236356
;     FILING DATE:  30-SEP-1994
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  JP 6-189274
;     FILING DATE:  11-AUG-1994
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  JP 6-189273
;     FILING DATE:  11-AUG-1945
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  JP 6-189272
;     FILING DATE:  11-AUG-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Resnick, David S.
;     REGISTRATION NUMBER:  34,235
;     REFERENCE/DOCKET NUMBER:  45753
;   TELECOMMUNICATION INFORMATION:
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   Query Match              61.6%;   Score 697.6;  DB 3;   Length 843;
   Best Local Similarity    89.9%;   Pred. No. 2.4e-157;
   Matches  748;  Conservative    0;  Mismatches   84;  Indels    0;  Gaps    0;


Qy       252 CATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCT 311
             | |   ||| ||||||| |||||| || || ||||||||| || |||||||||||||||| ||
Db         9 CGTGTTCATCCTGTCACTGGCCGATGTGCTGGTGACAGCCATCTGCCTGCCGGCCAGTCT 68


Qy       312 GCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTA 371
             |||||| ||||||||| || ||||||| || ||||||||||||||||||||||||||||||
Db        69 GCTGGTAGACATCACGGAATCCTGGCTCTTTGGCCATGCCCTCTGCAAGGTCATCCCCTA 128


Qy       372 TCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCG 431
             ||||||||| ||||||||||||||||| |||||| |||||| ||||||||| ||||||||||||
Db       129 TCTACAGGCCGTGTCCGTGTCAGTGGTCGTGCTGACTCTCAGCTCCATCGCCCTGGACCG 188


Qy       432 CTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTC 491
             |||||| ||||||||||||||| || ||||||||||||||| |||||||| |||||| |||||
Db       189 CTGGTACGCCATCTGCCACCCGCTGTTGTTCAAGAGCACTGCCCGGCGCGCCCGCGGCTC 248


Qy       492 CATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGA 551
             |||||| ||||||||||| ||||||||||| |||||||||| |||||||| ||||||||
Db       249 CATCCTCGGCATCTGGGCGGTGTCGCTGGCTGTCATGGTGCCTCAGGCTGCTGTCATGGA 308


Qy       552 ATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGA 611
             || |||||| ||||||| ||||| ||||||||| || ||| | || |||||||||||
Db       309 GTGTAGCAGCGTGCTGCCCGAGCTGGCCAACCGCACCCGCCTCCTGTCTGTCTGTGATGA 368


Qy       612 ACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTA 671
             ||||||||||| |||||| || ||||||||||||||||||| ||||||||| ||||||||||||
Db       369 GCGCTGGGCAGACGACCTGTACCCCAAGATCTACCACAGCTGCTTCTTCATTGTCACCTA 428


Qy       672 CCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGG 731
             |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db       429 CCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATCTTCCGCAAGCTCTGGGG 488


Qy       732 CCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCA 791
             ||||||||||||||||||||||||| || |||||||| |||||||||||| |||||||||||
Db       489 CCGCCAGATCCCCGGCACCACCTCGGCCCTGGTGCGCAACTGGAAGCGGCCCTCAGACCA 548


Qy       792 GCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCT 851
             |||||  |||| || ||||||||||  |||||||||||||||||| ||||||||||||
Db       549 GCTGGACGACCAGGGCCAGGGCCTGAGCTCAGAGCCCCAGCCCCGGGCCCGCGCCTTCCT 608
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Qy        852 GGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCT 911
              ||| || ||||| |||||||| || ||||||||||| ||||||||||||||||||||||||
Db        609 GGCCGAGGTGAAACAGATGCGAGCCCGGAGGAAGACGGCCAAGATGCTGATGGTGGTGCT 668

Qy        912 GCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTT 971
              |||||||||||||||||||||||||||||||||||| ||||||||| ||||| |||||||| ||
Db        669 GCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGTGTCCTCAACGTCCTCAAGAGGGTCTT 728

Qy        972 CGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCA 1031
              |||||||||||||||||||||| ||||| || || ||||||||||||||||||||||||||||
Db        729 CGGGATGTTCCGCCAAGCCAGCGACCGAGAGGCCATCTACGCCTGCTTCACCTTCTCCCA 788

Qy       1032 CTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTC 1083
              |||||||||||||||||||||||||||| ||||| ||| || ||||| |||||||
Db        789 CTGGCTGGTGTACGCCAACAGCGCCGCCAATCCCCTCCTCTACTCCTTCCTC 840
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RESULT 13
US-08-513-974B-55
; Sequence 55, Application US/08513974B
; Patent No. 6114139
;   GENERAL INFORMATION:
;   APPLICANT: Hinuma, Shuji
;   APPLICANT: Hosoya, Masaki
;   APPLICANT: Fujii, Ryo
;   APPLICANT: Ohtaki, Tetsuya
;   APPLICANT: Fukusumi, Shoji
;   APPLICANT: Ohgi, Kazuhiro
;   TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
;   TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
;   NUMBER OF SEQUENCES: 380
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;   STREET: 130 Water Street
;   CITY: Boston
;   STATE: MA
;   COUNTRY: USA
;   ZIP: 02109
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/513,974B
;   FILING DATE: 14-SEP-1995
;   CLASSIFICATION: 536
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/JP95/01599
;   FILING DATE: 10-AUG-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: JP 7-093989
;   FILING DATE: 19-AUG-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: JP 7-057186
;   FILING DATE: 16-MAR-1995
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  Query Match              59.2%;  Score 670.6;  DB 3;  Length 789;
  Best Local Similarity    90.6%;  Pred. No. 6.5e-151;
  Matches  715;  Conservative    0;  Mismatches   74;  Indels    0;  Gaps    0;

Qy       271 GCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGGACATCACTGAG 330
             || || ;| ||||||||| || ||||||||||||||||| |||||||| |||||||| ;|
Db         1 GCCGATGTGCTGGTGACAGCCATCTGCCTGCCGGCCAGTCTGCTGGTAGACATCACGGAA 60

Qy       331 TCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGGCTGTGTCCGTG 390
             |||||||| || |||||||||||||||||||||||||||||||||||||||| ||||||||
Db        61 TCCTGGCTCTTTGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGGCCGTGTCCGTG 120

Qy       391 TCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATGCCATCTGCCAC 450
             |||||||    |||||  ||||||||||| ||||||||||||||||||||  |||||||||||
Db       121 TCAGTGGTCGTGCTGACTCTCAGCTCCATCGCCCTGGACCGCTGGTACGCCATCTGCCAC 180

Qy       451 CCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGGGCATCTGGGCT 510
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Db    181 CCGCTGTTGTTCAAGAGCACTGCCCGGCGCGCCCGCGGCTCCATCCTCGGCATCTGGGCG 240

Qy    511 GTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCT 570
            ||||||||||||  ||||||||||  |||||||||  ||||||||  ||  ||||||  |||||||||
Db    241 GTGTCGCTGGCTGTCATGGTGCCTCAGGCTGCTGTCATGGAGTGTAGCAGCGTGCTGCCC 300

Qy    571 GAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTC 630
            |||||  |||||||||||  ||  |||  |  ||  |||||||||||  |||||||||||  |||||
Db    301 GAGCTGGCCAACCGCACCCGCCTCCTGTCTGTCTGTGATGAGCGCTGGGCAGACGACCTG 360

Qy    631 TATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTC 690
            ||  ||||||||||||||||||  |||||||||  ||||||||||||||||||||||||||||||||
Db    361 TACCCCAAGATCTACCACAGCTGCTTCTTCATTGTCACCTACCTGGCCCCACTGGGCCTC 420

Qy    691 ATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACC 750
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Db    421 ATGGCCATGGCCTATTTCCAGATCTTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACC 480

Qy    751 ACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGGACCTGGAGCAG 810
            |||||  ||  |||||||||  |||||||||||  ||||||||||||||||  ||||  ||  |||
Db    481 ACCTCGGCCCTGGTGCGCAACTGGAAGCGGCCCTCAGACCAGCTGGACGACCAGGGCCAG 540

Qy    811 GGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAGTGAAGCAGATG 870
            ||||||||  |||||||||||||||||  |||||||||||||  ||  ||||||  ||||||
Db    541 GGCCTGAGCTCAGAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCCGAGGTGAAACAGATG 600

Qy    871 CGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGC 930
            ||  ||  |||||||||||  |||||||||||||||||||||||||||||||||||||||||||||
Db    601 CGAGCCCGGAGGAAGACGGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGC 660

Qy    931 TACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCC 990
            |||||||||||||||  ||||||||  |||||  |||||||||  ||||||||||||||||||||||
Db    661 TACCTGCCCATCAGTGTCCTCAACGTCCTCAAGAGGGTCTTCGGGATGTTCCGCCAAGCC 720

Qy    991 AGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAAC 1050
            ||  |||||  ||  ||    |||||||||||||||||||||||||||||||||||||||||||||
Db    721 AGCGACCGAGAGGCCATCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAAC 780

Qy    1051 AGCGCTGCC 1059
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Db    781 AGCGCCGCC 789
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RESULT 14
US-09-461-436B-55
; Sequence 55, Application US/09461436B
; Patent No. 6538107
;   GENERAL INFORMATION:
;   APPLICANT: Shuji Hinuma
;   Yasuaki Ito
;   Ryo Fujii
;   TITLE OF INVENTION: G Protein Coupled Receptor Protein,
;   Production, And Use Thereof
;   NUMBER OF SEQUENCES: 61
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Edwards & Angell, LLP

;   STREET: 101 Federal Street
;   CITY: BOSTON
;   STATE: MA
;   COUNTRY: USA
;   ZIP: 02209
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/461,436B
;   FILING DATE: 14-Dec-1999
;   CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/513,974
;   FILING DATE: 14-SEP-1995
;   APPLICATION NUMBER: PCT/JP95/01599
;   FILING DATE: 10-AUG-1995
;   APPLICATION NUMBER: 7-093989
;   FILING DATE: 19-APR-1995
;   APPLICATION NUMBER: 7-057186
;   FILING DATE: 16-MAR-1995
;   APPLICATION NUMBER: 7-007177
;   FILING DATE: 20-JAN-1995
;   APPLICATION NUMBER: 6-326611
;   FILING DATE: 28-DEC-1994
;   APPLICATION NUMBER: 6-270017
;   FILING DATE: 02-NOV-1994
;   APPLICATION NUMBER: 6-236357
;   FILING DATE: 30-SEP-1994
;   APPLICATION NUMBER: 6-236356
;   FILING DATE: 30-SEP-1994
;   APPLICATION NUMBER: 6-189274
;   FILING DATE: 11-AUG-1994
;   APPLICATION NUMBER: 6-189273
;   FILING DATE: 11-AUG-1994
;   APPLICATION NUMBER: 6-189272
;   FILING DATE: 11-AUG-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: CONLIN, DAVID G.
;   REGISTRATION NUMBER: <Unknown>
;   REFERENCE/DOCKET NUMBER: 45753 DIV2
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 617-439-4444
;   TELEFAX: 617-439-4170
;   INFORMATION FOR SEQ ID NO: 55:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 789 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-09-461-436B-55

     Query Match   59.2%; Score 670.6; DB 4; Length 789;

Best Local Similarity   90.6%; Pred. No. 6.5e-151;
Matches   715; Conservative   0; Mismatches   74; Indels   0; Gaps   0;

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Qy    271 GCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGGACATCACTGAG 330
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Db      1 GCCGATGTGCTGGTGACAGCCATCTGCCTGCCGGCCAGTCTGCTGGTAGACATCACGGAA 60

Qy    331 TCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGGCTGTGTCCGTG 390
          ||||||||| ||  ||||||||||||||||||||||||||||||||||||||  |||||||||||
Db     61 TCCTGGCTCTTTGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGGCCGTGTCCGTG 120

Qy    391 TCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATGCCATCTGCCAC 450
          |||||||  ||||| |||||||||| ||||||||||||||||||||||||| |||||||||||||
Db    121 TCAGTGGTCGTGCTGACTCTCAGCTCCATCGCCCTGGACCGCTGGTACGCCATCTGCCAC 180

Qy    451 CCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGGGCATCTGGGCT 510
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Db    181 CCGCTGTTGTTCAAGAGCACTGCCCGGCGCGCCCGCGGCTCCATCCTCGGCATCTGGGCG 240

Qy    511 GTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCT 570
          ||||||||||||  ||||||||||  |||||||||  ||||||| ||  |||||  |||||||||
Db    241 GTGTCGCTGGCTGTCATGGTGCCTCAGGCTGCTGTCATGGAGTGTAGCAGCGTGCTGCCC 300

Qy    571 GAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTC 630
          ||||| |||||||||||| ||  ||| | || |||||||||||| |||||||||||| |||||
Db    301 GAGCTGGCCAACCGCACCCGCCTCCTGTCTGTCTGTGATGAGCGCTGGGCAGACGACCTG 360

Qy    631 TATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTC 690
          ||  |||||||||||||||||| |||||| | ||||||||||||||||| ||||||||||||
Db    361 TACCCCAAGATCTACCACAGCTGCTTCTTCATTGTCACCTACCTGGCCCCACTGGGCCTC 420

Qy    691 ATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACC 750
          ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db    421 ATGGCCATGGCCTATTTCCAGATCTTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACC 480

Qy    751 ACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGGACCTGGAGCAG 810
          ||||| || |||||||| |||||||||||| |||||||||||||||  |||| ||  |||
Db    481 ACCTCGGCCCTGGTGCGCAACTGGAAGCGGCCCTCAGACCAGCTGGACGACCAGGGCCAG 540

Qy    811 GGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAGTGAAGCAGATG 870
          ||||||||  |||||||||||||||||||||||||||||||||| ||  |||||  ||||||
Db    541 GGCCTGAGCTCAGAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCCGAGGTGAAACAGATG 600

Qy    871 CGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGC 930
          ||  ||  ||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db    601 CGAGCCCGGAGGAAGACGGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGC 660

Qy    931 TACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCC 990
          ||||||||||||||| ||||||| ||||| ||||||| |||||||||||||||||||||||
Db    661 TACCTGCCCATCAGTGTCCTCAACGTCCTCAAGAGGGTCTTCGGGATGTTCCGCCAAGCC 720

Qy    991 AGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAAC 1050
          ||  |||||| || ||  ||||||||||||||||||||||||||||||||||||||||||||
Db    721 AGCGACCGAGAGGCCATCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAAC 780

Qy   1051 AGCGCTGCC 1059
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Db   781 AGCGCCGCC 789

RESULT 15
US-09-119-788-1
; Sequence 1, Application US/09119788
; Patent No. 6166193
; GENERAL INFORMATION:
;   APPLICANT: Yanagisawa, Masashi
;   TITLE OF INVENTION: CDNA CLONE MY1 THAT ENCODES
;   TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
;   NUMBER OF SEQUENCES: 2
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: SmithKline Beecham Corporation
;   STREET: 709 Swedeland Road
;   CITY: King of Prussia
;   STATE: PA
;   COUNTRY: United States of America
;   ZIP: 19406
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/119,788
;   FILING DATE: 21-JUL-1998
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 60/053,790
;   FILING DATE: 25-JUL-1997
;   ATTORNEY/AGENT INFORMATION:
;   NAME: King, William T
;   REGISTRATION NUMBER: 30,954
;   REFERENCE/DOCKET NUMBER: GH50029
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 610-270-5515
;   TELEFAX: 610-270-5090
;   TELEX:
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1633 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: Genomic DNA
US-09-119-788-1

   Query Match   46.0%; Score 520.8; DB 3; Length 1633;
   Best Local Similarity 70.5%; Pred. No. 4.2e-115;
   Matches 712; Conservative   0; Mismatches 292; Indels   6; Gaps   1;

Qy   80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
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Db   217 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTGCACCCGAAAGAATATGAGT 276

Qy   140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199

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Db    277 GGGTCCTGATCGCCGGGTACATCATCGTGTTCGTCGTGGCTCTCATTGGGAACGTCCTGG 336

Qy    200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
            | ||  |||| ||||||  |||||||||||||||||||| || ||||||||||||| ||||
Db    337 TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA 396

Qy    260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
            | || || |||||||| || || |||||    | ||||| || |||| ||| | ||||
Db    397 ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCCAGCCACACTGGTCGTGG 456

Qy    320 ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG 379
            | ||||||||| |||||| | || || || ||  |||| ||||| || || || |||||||||
Db    457 ATATCACTGAGACCTGGTTTTTTGGACAGTCCCTTTGCAAAGTGATTCCTTATCTACAGA 516

Qy    380 CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATG 439
            | ||||| ||||| ||| | || || || || || |||| |||||| ||||| || |||||||||
Db    517 CCGTGTCGGTGTCTGTGTCTGTCCTCACACTGAGCTGTATCGCCTTGGATCGGTGGTATG 576

Qy    440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG 499
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Db    577 CAATCTGTCACCCTTTGATGTTTAAGAGCACAGCAAAGCGGGCCCGTAACAGCATTGTCA 636

Qy    500 GCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCA 559
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Db    637 TCATCTGGATTGTCTCCTGCATTATAATGATTCCTCAGGCCATCGTCATGGAGTGCAGCA 696

Qy    560 GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGG 619
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Db    697 CCGTGTTCCCAGGCTTAGCCAATAAAACCACCCTCTTTACGGTGTGTGATGAGCGCTGGG 756

Qy    620 CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCC 679
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Db    757 GTGGTGAAATTTATCCCAAGATGTACCACATCTGTTTCTTTCTGGTGACATACATGGCAC 816

Qy    680 CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA 739
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Db    817 CACTGTGTCTCATGGTGTTGGCTTATCTGCAAATATTTCGCAAACTCTGGTGTCGACAGA 876

Qy    740 TCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGG 799
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Db    877 TCCCTGGAACATCATCTGTAGTTCAGAGAAAATGGAAGCCCC------TGCAGCCTGTTT 930

Qy    800 ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAG 859
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Db    931 CACAGCCTCGAGGGCCAGGACAGCCAACGAAGTCCCGGATGGGCGCTGTGGCGGCTGAAA 990

Qy    860 TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCT 919
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Db    991 TAAAGCAGATCCGAGCCAGAAGGAAAACAGCCCGGATGTTGATGGTTGTGCTTTTGGTAT 1050

Qy    920 TCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGT 979
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Db   1051 TTGCAATTTGCTATCTACCAATTAGCATCCTCAATGTGCTAAAGAGAGTATTTGGGATGT 1110

Qy    980 TCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGG 1039
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Db       1111 TTGCCCATACTGAAGACAGAGAGACTGTGTATGCCTGGTTTACCTTTTCACACTGGCTTG 1170

Qy       1040 TGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGGA 1089
              | || |||||| || |||||| || || || || || || || |||||||||
Db       1171 TATATGCCAATAGTGCTGCGAATCCAATTATTTATAATTTTCTCAGTGGA 1220
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Search completed: October 15, 2004, 22:55:10
Job time : 90.8123 secs

OM nucleic - nucleic search, using sw model

Run on: October 15, 2004, 19:59:43 ; Search time 584.359 Seconds
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Title: US-10-070-532-5
Perfect score: 1133
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Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 3340653 seqs, 2534783454 residues

Total number of hits satisfying chosen parameters: 6681306

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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                 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
                 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
                 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
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                 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
                 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                 SUMMARIES
                      %
Result   Query

No.	Score	Match	Length	DB	ID	Description
1	1131.4	99.9	1133	10	US-09-393-696-5	Sequence 5, Appli
2	1114.4	98.4	1116	14	US-10-077-874-5	Sequence 5, Appli
3	1086.4	95.9	1564	15	US-10-225-567A-367	Sequence 367, App
4	1086.4	95.9	1564	16	US-10-352-684A-21	Sequence 21, Appl
5	1084.8	95.7	1110	14	US-10-077-874-3	Sequence 3, Appli
6	1084.8	95.7	1209	14	US-10-077-874-1	Sequence 1, Appli
7	1084.8	95.7	1564	9	US-09-828-538-23	Sequence 23, Appl
8	1081.6	95.5	1209	10	US-09-393-696-1	Sequence 1, Appli
9	1081.6	95.5	1278	11	US-09-826-509-548	Sequence 548, App
10	1076.8	95.0	1110	10	US-09-393-696-3	Sequence 3, Appli
11	912	80.5	1281	9	US-09-730-931-1	Sequence 1, Appli
12	670.6	59.2	789	15	US-10-278-087A-55	Sequence 55, Appl
13	520.8	46.0	1633	15	US-10-282-717-1	Sequence 1, Appli
14	520.8	46.0	1843	15	US-10-225-567A-369	Sequence 369, App
15	516	45.5	1335	11	US-09-826-509-550	Sequence 550, App
16	249.2	22.0	9785	9	US-09-961-848-1	Sequence 1, Appli
17	249.2	22.0	10453	9	US-09-828-538-21	Sequence 21, Appl
18	244	21.5	244	9	US-09-828-538-6	Sequence 6, Appli
19	225.4	19.9	227	9	US-09-828-538-10	Sequence 10, Appl
20	197.4	17.4	356	9	US-09-828-538-2	Sequence 2, Appli
21	179	15.8	179	9	US-09-828-538-4	Sequence 4, Appli
22	163.2	14.4	1290	17	US-10-719-587-55	Sequence 55, Appl
23	163.2	14.4	1290	17	US-10-719-587-56	Sequence 56, Appl
24	163.2	14.4	1293	9	US-09-866-248A-7	Sequence 7, Appli
25	163.2	14.4	1293	15	US-10-225-567A-657	Sequence 657, App
26	163.2	14.4	1320	9	US-09-292-973-3	Sequence 3, Appli
27	156.2	13.8	1299	17	US-10-719-587-38	Sequence 38, Appl
28	156.2	13.8	1410	9	US-09-866-248A-1	Sequence 1, Appli
29	149.8	13.2	1532	9	US-09-292-973-1	Sequence 1, Appli
30	128.4	11.3	168575	15	US-10-178-194-1	Sequence 1, Appli
31	124.4	11.0	977	12	US-09-876-143-1561	Sequence 1561, Ap
32	122	10.8	122	9	US-09-828-538-12	Sequence 12, Appl
33	120.6	10.6	1174	17	US-10-611-210-9	Sequence 9, Appli
34	119.8	10.6	1174	17	US-10-611-210-7	Sequence 7, Appli
35	119	10.5	1110	14	US-10-044-592-17	Sequence 17, Appl
36	119	10.5	1110	15	US-10-278-087A-31	Sequence 31, Appl
37	119	10.5	1113	15	US-10-225-567A-244	Sequence 244, App
38	119	10.5	1152	17	US-10-611-210-10	Sequence 10, Appl
39	119	10.5	1331	14	US-10-044-592-73	Sequence 73, Appl
40	118.4	10.5	1173	17	US-10-611-210-6	Sequence 6, Appli
41	116	10.2	116	9	US-09-828-538-8	Sequence 8, Appli
42	115.8	10.2	1174	17	US-10-611-210-8	Sequence 8, Appli
43	107.2	9.5	669	14	US-10-044-592-70	Sequence 70, Appl
c 44	105.6	9.3	436	13	US-10-027-632-275272	Sequence 275272,
c 45	105.6	9.3	436	16	US-10-027-632-275272	Sequence 275272,

ALIGNMENTS

RESULT 1
US-09-393-696-5
; Sequence 5, Application US/09393696
; Publication No. US20030022277A1
; GENERAL INFORMATION:

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  Query Match              99.9%;   Score 1131.4;   DB 10;   Length 1133;
  Best Local Similarity    99.9%;   Pred. No. 0;
  Matches 1132;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;


Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGACCCC 60


Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120


Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180


Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240


Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300


Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360


Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420


Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480


Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Db      481   GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy      541   GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541   GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy      601   GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601   GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy      661   ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661   ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy      721   AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721   AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy      781   CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781   CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy      841   CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841   CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy      901   ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901   ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy      961   AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961   AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy      1021  ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021  ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy      1081  CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG 1133
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081  CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG 1133
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RESULT 2
US-10-077-874-5
; Sequence 5, Application US/10077874
; Publication No. US20020115155A1
;   GENERAL INFORMATION:
;   APPLICANT: Soppet, Daniel et al
;   TITLE OF INVENTION: Human Neuropeptide Receptor
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Human Genome Sciences, Inc.
;   STREET: 9410 Key West Avenue
;   CITY: Rockville
;   STATE: MD

    Query Match   98.4%;   Score 1114.4; DB 14;   Length 1116;
    Best Local Similarity   99.9%;   Pred. No. 6.2e-311;
    Matches 1115; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGACCCC 60

Qy   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

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Qy     301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy     361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy     421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy     481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy     541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy     601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy     661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy     721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy     781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy     841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy     901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy     961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy    1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy    1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCC 1116
           ||||||||||||||||||||||||||||||||||||
Db    1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCC 1116
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RESULT 3
US-10-225-567A-367
; Sequence 367, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED
RECEPTORS (GPCRS)
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 367
; LENGTH: 1564
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-367

  Query Match   95.9%; Score 1086.4; DB 15; Length 1564;
  Best Local Similarity   99.9%; Pred. No. 8e-303;
  Matches 1087; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy   301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy   361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

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Qy     421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy     481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy     541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy     601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy     661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy     721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy     781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy     841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy     901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
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Db    1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy     961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy    1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy    1081 CTCAGTGG 1088
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Db    1234 CTCAGTGG 1241
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    Query Match               95.9%;  Score 1086.4;  DB 16;  Length 1564;
    Best Local Similarity     99.9%;  Pred. No. 8e-303;
    Matches 1087;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy        61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy       121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      274  TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy      181  CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      334  CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy      241  ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      394  ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy      301  CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      454  CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy      361  GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      514  GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy      421  GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      574  GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy      481  GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      634  GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy      541  GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      694  GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy      601  GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      754  GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy      661  ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      814  ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy      721  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      874  AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy      781  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      934  CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGCAGAGCCCCAGCCCCGGGGC 993

Qy      841  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      994  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy      901  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy      961  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Db     1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy     1081 CTCAGTGG 1088
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Db     1234 CTCAGTGG 1241
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RESULT 5
US-10-077-874-3
; Sequence 3, Application US/10077874
; Publication No. US20020115155A1
;   GENERAL INFORMATION:
;   APPLICANT: Soppet, Daniel et al
;   TITLE OF INVENTION: Human Neuropeptide Receptor
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Human Genome Sciences, Inc.
;   STREET: 9410 Key West Avenue
;   CITY: Rockville
;   STATE: MD
;   COUNTRY: USA
;   ZIP: 20850
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/077,874
;   FILING DATE: 20-Feb-2002
;   CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/462,509
;   FILING DATE: 05-JUNE-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Wales, Michele M.
;   REGISTRATION NUMBER: 43,975
;   REFERENCE/DOCKET NUMBER: PF168P1D1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 301-309-8504
;   TELEFAX: 301-309-8439
;   INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1110 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 1..1110
;   SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-077-874-3
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Query Match              95.7%;   Score 1084.8;  DB 14;   Length 1110;
Best Local Similarity    99.8%;   Pred. No. 2.1e-302;
Matches 1086;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy    121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Qy      781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
            |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960

Qy      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy     1081 CTCAGTGG 1088
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Db     1081 CTCAGTGG 1088
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RESULT 6
US-10-077-874-1
; Sequence 1, Application US/10077874
; Publication No. US20020115155A1
;   GENERAL INFORMATION:
;   APPLICANT: Soppet, Daniel et al
;   TITLE OF INVENTION: Human Neuropeptide Receptor
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Human Genome Sciences, Inc.
;   STREET: 9410 Key West Avenue
;   CITY: Rockville
;   STATE: MD
;   COUNTRY: USA
;   ZIP: 20850
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/077,874
;   FILING DATE: 20-Feb-2002
;   CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/462,509
;   FILING DATE: 05-JUNE-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Wales, Michele M.
;   REGISTRATION NUMBER: 43,975
;   REFERENCE/DOCKET NUMBER: PF168P1D1
;   TELECOMMUNICATION INFORMATION:
```

Query Match                95.7%;   Score 1084.8;   DB 14;   Length 1209;
Best Local Similarity      99.8%;   Pred. No. 2.2e-302;
Matches 1086;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
            ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy      421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy      541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Db      541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy      601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy      661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy      721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy      781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db      781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840

Qy      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy     1081 CTCAGTGG 1088
            ||||||||
Db     1081 CTCAGTGG 1088


RESULT 7
US-09-828-538-23
; Sequence 23, Application US/09828538
; Patent No. US20010025031A1
; GENERAL INFORMATION:
;  APPLICANT: Ellis, Catherine E.
;  APPLICANT:  Kwok, Cheni
;  APPLICANT:  Bodsworth, Nicola J.
;  APPLICANT:  Halsey, Wendy
;  APPLICANT:  Van Horn, Stephanie
;  TITLE OF INVENTION: HFGAN72 Receptor Genomic DNA and Methods
;  TITLE OF INVENTION:  of Use Thereof in Diagnostic Applications
;  FILE REFERENCE: GH-50038-C1
;  CURRENT APPLICATION NUMBER: US/09/828,538
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: 60/088,624
;  PRIOR FILING DATE: 1998-06-08
;  PRIOR APPLICATION NUMBER: 60/093,726
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Query Match   95.7%; Score 1084.8; DB 9; Length 1564;
Best Local Similarity 99.8%; Pred. No. 2.3e-302;
Matches 1086; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

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Qy       1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
           |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db     214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGCGATTATCTG 273

Qy     121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy     181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy     241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy     301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy     361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy     421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy     481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy     541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy     601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081 CTCAGTGG 1088
              ||||||||
Db       1234 CTCAGTGG 1241


RESULT 8
US-09-393-696-1
; Sequence 1, Application US/09393696
; Publication No. US20030022277A1
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc. et al.
;  TITLE OF INVENTION: Human Neuropeptide Receptor
;  FILE REFERENCE: PF168P2
;  CURRENT APPLICATION NUMBER: US/09/393,696
;  CURRENT FILING DATE: 1999-09-10
;  EARLIER APPLICATION NUMBER: PCT/US95/05616
;  EARLIER FILING DATE: 1995-05-05
;  EARLIER APPLICATION NUMBER: US08/462,509
;  EARLIER FILING DATE: 1995-06-05
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 1209
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
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    Query Match   95.5%; Score 1081.6; DB 10; Length 1209;
    Best Local Similarity   99.6%; Pred. No. 1.8e-301;
    Matches 1084; Conservative   0; Mismatches   4; Indels   0; Gaps   0;

Qy   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy   121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
           ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   121 TACCCAAAACAGTATGAGTGGGTCCTCATCCCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy   301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy   361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy   421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy   481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy   541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy   601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
           |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy   661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy   721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
           || |||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Db        721 AACCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
                                                            (
Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGG 1088
              ||||||||
Db       1081 CTCAGTGG 1088
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RESULT 9
US-09-826-509-548
; Sequence 548, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
;   APPLICANT: Lehmann-Bruinsma, Karin
;   APPLICANT: Liaw, Chen W.
;   APPLICANT: Lin, I-Lin
;   TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated
Known G
;   TITLE OF INVENTION: Protein-Coupled Receptors
;   FILE REFERENCE: AREN-207
;   CURRENT APPLICATION NUMBER: US/09/826,509
;   CURRENT FILING DATE: 2001-04-05
;   PRIOR APPLICATION NUMBER: 60/195,747
;   PRIOR FILING DATE: 2000-04-07
;   PRIOR APPLICATION NUMBER: 09/170,496
;   PRIOR FILING DATE: 1998-10-13
;   NUMBER OF SEQ ID NOS: 589
;   SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 548
;   LENGTH: 1278
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-826-509-548

  Query Match   95.5%; Score 1081.6; DB 11; Length 1278;
  Best Local Similarity   99.6%; Pred. No. 1.8e-301;
  Matches 1084; Conservative   0; Mismatches   4; Indels   0; Gaps   0;

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Qy      1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC  60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG  60

Qy     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy    121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy    361 GTCATCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTCATCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy    841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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                 |||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db        841  CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAAAAAAGATGCTG 900

Qy        901  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901  ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961  AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021  ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021  ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081  CTCAGTGG 1088
                 ||||||||
Db       1081  CTCAGTGG 1088


RESULT 10
US-09-393-696-3
; Sequence 3, Application US/09393696
; Publication No. US20030022277A1
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc. et al.
;  TITLE OF INVENTION: Human Neuropeptide Receptor
;  FILE REFERENCE: PF168P2
;  CURRENT APPLICATION NUMBER: US/09/393,696
;  CURRENT FILING DATE: 1999-09-10
;  EARLIER APPLICATION NUMBER: PCT/US95/05616
;  EARLIER FILING DATE: 1995-05-05
;  EARLIER APPLICATION NUMBER: US08/462,509
;  EARLIER FILING DATE: 1995-06-05
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1110
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1110)
US-09-393-696-3

   Query Match            95.0%;  Score 1076.8;  DB 10;  Length 1110;
   Best Local Similarity  99.4%;  Pred. No. 4.3e-300;
   Matches 1081;  Conservative   0;  Mismatches   7;  Indels   0;  Gaps   0;

Qy          1  ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db          1  ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy         61  TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61  TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Qy    121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
          |||||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||
Db    541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy    841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy    901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
          |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db    901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960

Qy    961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy   1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy   1081 CTCAGTGG 1088
          ||||||||
Db   1081 CTCAGTGG 1088
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RESULT 11
US-09-730-931-1
; Sequence 1, Application US/09730931
; Patent No. US20020064814A1
; GENERAL INFORMATION:
; APPLICANT: ELLIS, CATHERINE E.
; TITLE OF INVENTION: DOG OREXIN 1 RECEPTOR
; FILE REFERENCE: GH-70669
; CURRENT APPLICATION NUMBER: US/09/730,931
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/169,373
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 1281
;   TYPE: DNA
;   ORGANISM: CANIS FAMILIARIS
US-09-730-931-1

   Query Match   80.5%;   Score 912;   DB 9;   Length 1281;
   Best Local Similarity 90.3%;   Pred. No. 1.5e-252;
   Matches 988; Conservative   0; Mismatches 100; Indels   6; Gaps   1;

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Qy      1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCC 60
          |||||||||||||||||||||||||||||||||||  |||   |||| | ||| || | ||||
Db      1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGACTGGGACCCCCACCGGCGGCGGGGAGCTG 60

Qy     61 TCCCCT------GTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGAT 114
          || ||       ||||||||| ||||||||||| ||||| || |||||||||||||| |||
Db     61 TCTCCGTCACTGGTGCCTCCCGACTATGAAGACGAGTTCCTGCGCTATCTGTGGCGCGAT 120

Qy    115 TATCTGTACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTC 174
          || ||||||||||| ||||||||||||||||||||||| ||| |||||||||||||||| |
Db    121 TACCTGTACCCAAAGCAGTATGAGTGGGTCCTCATCGCTGCCTACGTGGCTGTGTTCCTA 180

Qy    175 GTGGCCCTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGG 234
          |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db    181 GTGGCCCTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGAGGAACCACCACATGAGG 240

Qy    235 ACAGTCACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATC 294
          || |||||||||| ||||||||||||||||||||||||||| || ||||||| || |||
Db    241 ACGGTCACCAACTATTTCATTGTCAACCTGTCCCTGGCTGATGTGCTGGTGACAGCCATC 300

Qy    295 TGCCTGCCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTC 354
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                   |||||  |||||||||||||||||| ||||||||||||||||||||| ||||| ||| |||||
Db     301 TGCCTCCCGGCCAGCCTGCTGGTAGACATCACTGAGTCCTGGCTCTTCGGTCATACCCTC 360

Qy     355 TGCAAGGTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGC 414
                   ||||| |||||||||| |||||||| ||||| ||||| |||||||||| ||||||||||
Db     361 TGCAAAGTCATCCCCTACCTACAGGCCGTGTCTGTGTCGGTGGCAGTGCTGACTCTCAGC 420

Qy     415 TTCATCGCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCC 474
                   |||||||||||||||||||||||||||||||||||||||| || ||||||||||||| |||
Db     421 TTCATCGCCCTGGACCGCTGGTATGCCATCTGCCACCCGCTGTTGTTCAAGAGCACCGCC 480

Qy     475 CGGCGGGCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCC 534
                   |||||  |||||  |||||||||||||||||||||||||||||  ||||  |||||||| ||
Db     481 CGGCGCGCCCGCAGCTCCATCCTGGGCATCTGGGCTGTGTCATTGGCTGTCATGGTACCT 540

Qy     535 CAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTC 594
                   |||||||| |||||||||||||||||||| ||||| ||||||||||||||||||||| || |||
Db     541 CAGGCTGCCGTCATGGAATGCAGCAGCGTGCTCCCTGAGCTAGCCAACCGCACCCGCCTC 600

Qy     595 TTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGC 654
                   |||||  ||  |||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db     601 TTCTCTGTGTGTGATGAACACTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGC 660

Qy     655 TTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATA 714
                   |||||  ||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db     661 TTCTTCATTGTCACCTACTTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATC 720

Qy     715 TTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGG 774
                   |||||||||||||||||||||||||||||||||||| |||||||| || || ||||||| ||||||||
Db     721 TTCCGCAAGCTCTGGGGCCGCCAGATCCCTGGCACCACATCGGCCCTGGTGAGGAACTGG 780

Qy     775 AAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCC 834
                   |||||  |||||  ||||||||||  |||||  ||  ||  ||||||||| | ||  |||| ||
Db     781 AAGCGGCCCTCGGACCAGCTGGAGGACCAGGGGCCCGGCCTGAGCGCGGAACCCCCCCCT 840

Qy     835 CGGGGCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAG 894
                   ||||  |||  |||||||||||||||| |||||||||||||| ||  ||||||||||| ||||||
Db     841 CGGGGCCCGGGCCTTCCTGGCTGAGGTGAAGCAGATGCGAGCGCGGAGGAAGACGGCCAAG 900

Qy     895 ATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAAT 954
                   |||||||||||| |||||||||||||| |||||||||||||||||||||||||||| |||||||||
Db     901 ATGCTGATGGTGCTGCTGCTGGTCTTTGCCCTCTGCTACCTGCCCATCAGTGTCCTCAAT 960

Qy     955 GTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCC 1014
                   ||||| |||||||||||||||||||||||||||||| |||||||||| ||||| || ||||||
Db     961 GTCCTCAAGAGGGTGTTCGGGATGTTCCGCCAATCCAGTGACCGAGAAGCCGTGTACGCC 1020

Qy    1015 TGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTAC 1074
                   |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db    1021 TGCTTCACCTTCTCCCACTGGCTGGTGTATGCCAACAGCGCTGCCAACCCCATCATCTAC 1080

Qy    1075 AACTTCCTCAGTGG 1088
                   |||||||||| ||
Db    1081 AACTTCCTCAGCGG 1094


RESULT 12
```

; Sequence 55, Application US/10278087A
; Publication No. US20030138817A1
;   GENERAL INFORMATION:
;   APPLICANT: Shuji Hinuma
;   Yasuaki Ito
;   Ryo Fujii
;   TITLE OF INVENTION: G Protein Coupled Receptor Protein,
;   Production, And Use Thereof
;   NUMBER OF SEQUENCES: 61
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Edwards & Angell, LLP
;   STREET: 101 Federal Street
;   CITY: BOSTON
;   STATE: MA
;   COUNTRY: USA
;   ZIP: 02209
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/278,087A
;   FILING DATE: 31-Jan-2003
;   CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 09/461,436
;   FILING DATE: 14-DEC-1999
;   APPLICATION NUMBER: 09/038,572
;   FILING DATE: 11-MAR-1998
;   APPLICATION NUMBER: 08/513,974
;   FILING DATE: 14-SEP-1995
;   APPLICATION NUMBER: PCT/JP95/01599
;   FILING DATE: 10-AUG-1995
;   APPLICATION NUMBER: 7-093989
;   FILING DATE: 19-APR-1995
;   APPLICATION NUMBER: 7-057186
;   FILING DATE: 16-MAR-1995
;   APPLICATION NUMBER: 7-007177
;   FILING DATE: 20-JAN-1995
;   APPLICATION NUMBER: 6-326611
;   FILING DATE: 28-DEC-1994
;   APPLICATION NUMBER: 6-270017
;   FILING DATE: 02-NOV-1994
;   APPLICATION NUMBER: 6-236357
;   FILING DATE: 30-SEP-1994
;   APPLICATION NUMBER: 6-236356
;   FILING DATE: 30-SEP-1994
;   APPLICATION NUMBER: 6-189274
;   FILING DATE: 11-AUG-1994
;   APPLICATION NUMBER: 6-189273
;   FILING DATE: 11-AUG-1994
;   APPLICATION NUMBER: 6-189272
;   FILING DATE: 11-AUG-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: CONLIN, DAVID G.

```
   Query Match              59.2%;   Score 670.6;  DB 15;  Length 789;
   Best Local Similarity    90.6%;   Pred. No. 5.4e-183;
   Matches  715;  Conservative    0;  Mismatches   74;  Indels    0;  Gaps    0;


Qy        271 GCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGGACATCACTGAG 330
              || || || |||||||| || ||||||||||||||||| |||||||| |||||||| ||
Db          1 GCCGATGTGCTGGTGACAGCCATCTGCCTGCCGGCCAGTCTGCTGGTAGACATCACGGAA 60


Qy        331 TCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGGCTGTGTCCGTG 390
              |||||||| || |||||||||||||||||||||||||||||||||||| |||||||||||
Db         61 TCCTGGCTCTTTGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGGCCGTGTCCGTG 120


Qy        391 TCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATGCCATCTGCCAC 450
              ||||||| |||||· |||||||||| ||||||||||||||||||| |||||||||||||
Db        121 TCAGTGGTCGTGCTGACTCTCAGCTCCATCGCCCTGGACCGCTGGTACGCCATCTGCCAC 180


Qy        451 CCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGGGCATCTGGGCT 510
              || || ||||||||||||||| ||||||||| |||||| |||||||||| |||||||||
Db        181 CCGCTGTTGTTCAAGAGCACTGCCCGGCGCGCCCGCGGCTCCATCCTCGGCATCTGGGCG 240


Qy        511 GTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCT 570
              ||||||||||| |||||||||| ||||||||| |||||||| || ||||| ||||||||
Db        241 GTGTCGCTGGCTGTCATGGTGCCTCAGGCTGCTGTCATGGAGTGTAGCAGCGTGCTGCCC 300


Qy        571 GAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTC 630
              ||||| ||||||||||| || || ||| | || ||||||||||| ||||||||| |||||
Db        301 GAGCTGGCCAACCGCACCCGCCTCCTGTCTGTCTGTGATGAGCGCTGGGCAGACGACCTG 360


Qy        631 TATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTC 690
              || |||||||||||||||||| |||||||| ||||||||||||||||||| |||||··|||
Db        361 TACCCĆAAGATCTACCACAGCTGCTTCTTCATTGTCACCTACCTGGCCCCACTGGGĆCTC 420


Qy        691 ATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACC 750
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        421 ATGGCCATGGCCTATTTCCAGATCTTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACC 480


Qy        751 ACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGGACCTGGAGCAG 810
              ||||| || |||||||| |||||||||||| ||||||||||||||||| |||| || |||
Db        481 ACCTCGGCCCTGGTGCGCAACTGGAAGCGGCCCTCAGACCAGCTGGACGACCAGGGCCAG 540


Qy        811 GGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAGTGAAGCAGATG 870
              ||||||||    |||||||||||||||| ||||||||||||||| || ||||| ||||||
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Db       541  GGCCTGAGCTCAGAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCCGAGGTGAAACAGATG  600

Qy       871  CGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGC  930
              || || ||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       601  CGAGCCCGGAGGAAGACGGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGC  660

Qy       931  TACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCC  990
              ||||||||||||| ||||||||| ||||| ||||||||| ||||||||||||||||||||
Db       661  TACCTGCCCATCAGTGTCCTCAACGTCCTCAAGAGGGTCTTCGGGATGTTCCGCCAAGCC  720

Qy       991  AGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAAC  1050
              || |||||| || || |||||||||||||||||||||||||||||||||||||||||||||
Db       721  AGCGACCGAGAGGCCATCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAAC  780

Qy      1051  AGCGCTGCC  1059
              ||||| |||
Db       781  AGCGCCGCC  789


RESULT 13
US-10-282-717-1
; Sequence 1, Application US/10282717
; Publication No. US20030083466A1
; GENERAL INFORMATION:
;  APPLICANT: YANAGISAWA, MASASHI
;  TITLE OF INVENTION: cDNA CLONE MY1 THAT ENCODES A NOVEL
;  TITLE OF INVENTION:  HUMAN 7-TRANSMEMBRANE RECEPTOR
;  FILE REFERENCE: GH50029D1C1
;  CURRENT APPLICATION NUMBER: US/10/282,717
;  CURRENT FILING DATE:  2002-10-28
;  PRIOR APPLICATION NUMBER: 09/676,625
;  PRIOR FILING DATE: 2000-10-02
;  PRIOR APPLICATION NUMBER: 09/119,788
;  PRIOR FILING DATE: 1998-07-21
;  PRIOR APPLICATION NUMBER: 60/053,790
;  PRIOR FILING DATE: 1997-07-25
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 1633
;   TYPE: DNA
;   ORGANISM: HOMO SAPIENS
US-10-282-717-1

  Query Match           46.0%;  Score 520.8;  DB 15;  Length 1633;
  Best Local Similarity  70.5%;  Pred. No. 1e-139;
  Matches  712;  Conservative  0;  Mismatches  292;  Indels  6;  Gaps  1;

Qy        80  ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT  139
              | || || || || || || || || ||||||| | || || ||| |||| ||| | |||||||
Db       217  ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTGCACCCGAAAGAATATGAGT  276

Qy       140  GGGTCCTCATCGCAGCCTATGTGGCTGTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG  199
              ||||||| |||||| | || | |||||||||||| || | || ||| |||
Db       277  GGGTCCTGATCGCCGGGTACATCATCGTGTTCGTCGTGGCTCTCATTGGGAACGTCCTGG  336

Qy       200  TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA  259
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                    | ||   |||| ||||||  ||||||||||||||||||| || |||||||||||||| ||||
Db   337 TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA 396

Qy   260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
                    | ||  || |||||||||| || || |||||    | ||||||| || |||| ||| | ||||
Db   397 ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCCAGCCACACTGGTCGTGG 456

Qy   320 ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG 379
                    | |||||||||| ||||| | || || ||  |||| ||||| || || || |||||||||
Db   457 ATATCACTGAGACCTGGTTTTTTGGACAGTCCCTTTGCAAAGTGATTCCTTATCTACAGA 516

Qy   380 CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATG 439
                    | ||||| ||||| ||| | || || || || |||| |||||| |||| || |||||||
Db   517 CCGTGTCGGTGTCTGTGTCTGTCCTCACACTGAGCTGTATCGCCTTGGATCGGTGGTATG 576

Qy   440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG 499
                    | |||||| |||||| |    |||| |||||||||| ||||||||| | | ||| |
Db   577 CAATCTGTCACCCTTTGATGTTTAAGAGCACAGCAAAGCGGGCCCGTAACAGCATTGTCA 636

Qy   500 GCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCA 559
                    ||||||| ||| ||          || ||| | || |||||      |||||||| |||||||
Db   637 TCATCTGGATTGTCTCCTGCATTATAATGATTCCTCAGGCCATCGTCATGGAGTGCAGCA 696

Qy   560 GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGG 619
                    ||| | || |       |||||||   ||       ||||| | ||| ||||||||| |||||||
Db   697 CCGTGTTCCCAGGCTTAGCCAATAAAACCACCCTCTTTACGGTGTGTGATGAGCGCTGGG 756

Qy   620 CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCC 679
                    | |||  | ||||||||||| ||||||| || |||||| | || || ||| |||| |
Db   757 GTGGTGAAATTTATCCCAAGATGTACCACATCTGTTTCTTTCTGGTGACATACATGGCAC 816

Qy   680 CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA 739
                    ||||| | ||||||     |||| ||| | || ||||| ||||| |||||| | || ||||
Db   817 CACTGTGTCTCATGGTGTTGGCTTATCTGCAAATATTTCGCAAACTCTGGTGTCGACAGA 876

Qy   740 TCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGG 799
                    |||| || ||  | || | |     | | || ||||||| ||           |||| |
Db   877 TCCCTGGAACATCATCTGTAGTTCAGAGAAAATGGAAGCCCC------TGCAGCCTGTTT 930

Qy   800 ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAG 859
                    | |   | || |   |        | || ||||| |||| |     |||||||
Db   931 CACAGCCTCGAGGGCCAGGACAGCCAACGAAGTCCCGGATGGGCGCTGTGGCGGCTGAAA 990

Qy   860 TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCT 919
                    | |||||||| || || | ||||| |||||| |||| ||||||| ||||| |||| |
Db   991 TAAAGCAGATCCGAGCCAGAAGGAAAACAGCCCGGATGTTGATGGTTGTGCTTTTGGTAT 1050

Qy   920 TCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGT 979
                    | || | ||||| || || || ||| ||||||||||| || ||||| || || |||||||
Db  1051 TTGCAATTTGCTATCTACCAATTAGCATCCTCAATGTGCTAAAGAGAGTATTTGGGATGT 1110

Qy   980 TCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGG 1039
                    |  ||| |   ||| | || |||| || ||||| || ||||| || |||||||||| |
Db  1111 TTGCCCATACTGAAGACAGAGAGACTGTGTATGCCTGGTTTACCTTTTCACACTGGCTTG 1170

Qy  1040 TGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGGA 1089
                    | || |||||| || ||||| || || || || || || || |||||||||
```

RESULT 14
US-10-225-567A-369
; Sequence 369, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED
RECEPTORS (GPCRS)
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 369
; LENGTH: 1843
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-369

    Query Match   46.0%; Score 520.8; DB 15; Length 1843;
    Best Local Similarity   70.5%; Pred. No. 1e-139;
    Matches 712; Conservative   0; Mismatches 292; Indels   6; Gaps   1;

Qy   80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
            | || || || || || || || || |||||| | || || ||| |||| ||| | |||||||
Db   428 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTGCACCCGAAAGAATATGAGT 487

Qy   140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
            ||||||| |||||| | || | ||||||||||||||| || | || ||| |||
Db   488 GGGTCCTGATCGCCGGGTACATCATCGTGTTCGTCGTGGCTCTCATTGGGAACGTCCTGG 547

Qy   200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
            | || |||| |||||| |||||||||||||||||||||| || |||||||||||||| ||||
Db   548 TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA 607

Qy   260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
            | || || |||||||| || || ||||| | ||||||| || |||| ||| | ||||
Db   608 ATCTTTCTCTGGCTGATGTGCGTCGTGACCATCACCTGCCTTCCAGCCACACTGGTCGTGG 667

Qy   320 ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG 379
            | |||||||| ||||| | || || || |||| ||||| || || || || |||||||||
Db   668 ATATCACTGAGACCTGGTTTTTTTGGACAGTCCCTTTGCAAAGTGATTCCTTATCTACAGA 727

Qy   380 CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATG 439
            | |||||| ||||| ||| | || || || || || |||| ||||||| |||| || |||||||
Db   728 CCGTGTCGGTGTCTGTGTCTGTCCTCACACTGAGCTGTATCGCCTTGGATCGGTGGTATG 787

Qy   440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG 499
            | |||||| ||||| | |||| |||||||||||| |||||||||| | ||| |

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Db          788 CAATCTGTCACCCTTTGATGTTTAAGAGCACAGCAAAGCGGGCCCGTAACAGCATTGTCA 847

Qy          500 GCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCA 559
                |||||||   |||  ||      || ||| |  || |||||     |||||||| |||||||
Db          848 TCATCTGGATTGTCTCCTGCATTATAATGATTCCTCAGGCCATCGTCATGGAGTGCAGCA 907

Qy          560 GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGG 619
                ||| | || |  |||||||    ||    ||||| | || ||||||||| |||||||
Db          908 CCGTGTTCCCAGGCTTAGCCAATAAAACCACCCTCTTTACGGTGTGTGATGAGCGCTGGG 967

Qy          620 CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCC 679
                |  |||  | |||||||||||| |||||||  || |||||| | || || ||| |||| |
Db          968 GTGGTGAAATTTATCCCAAGATGTACCACATCTGTTTCTTTCTGGTGACATACATGGCAC 1027

Qy          680 CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA 739
                ||||| | ||||||||    |||| ||| | || ||||| ||||| |||||| | || ||||
Db         1028 CACTGTGTCTCATGGTGTTGGCTTATCTGCAAATATTTCGCAAACTCTGGTGTCGACAGA 1087

Qy          740 TCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGG 799
                |||| || ||  | || | |    | | || |||||||| ||           ||||  |
Db         1088 TCCCTGGAACATCATCTGTAGTTCAGAGAAAATGGAAGCCCC------TGCAGCCTGTTT 1141

Qy          800 ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAG 859
                | |   | ||| |     | || ||||     |||| |   |||||||
Db         1142 CACAGCCTCGAGGGCCAGGACAGCCAACGAAGTCCCGGATGAGCGCTGTGGCGGCTGAAA 1201

Qy          860 TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCT 919
                | |||||||||| || ||  | | ||||| |||||| |||| ||||||| ||||| |||| |
Db         1202 TAAAGCAGATCCGAGCCAGAAGGAAAACAGCCCGGATGTTGATGGTTGTGCTTTTGGTAT 1261

Qy          920 TCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGT 979
                | ||  | ||||| ||  || || || ||| ||||||||||||| || ||||| || || ||||||||
Db         1262 TTGCAATTTGCTATCTACCAATTAGCATCCTCAATGTGCTAAAGAGAGTATTTGGGATGT 1321

Qy          980 TCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGG 1039
                |    ||| |     ||| | || ||||  || ||||| || |||| || ||||||||| |
Db         1322 TTGCCCATACTGAAGACAGAGAGACTGTGTATGCCTGGTTTACCTTTTCACACTGGCTTG 1381

Qy         1040 TGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGGA 1089
                | || ||||| || ||||| || || || || || ||| || ||||||||||
Db         1382 TATATGCCAATAGTGCTGCGAATCCAATTATTTATAATTTTCTCAGTGGA 1431
```

RESULT 15
US-09-826-509-550
; Sequence 550, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated
Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05

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  Query Match              45.5%;  Score 516;  DB 11;  Length 1335;
  Best Local Similarity    70.2%;  Pred. No. 2.3e-138;
  Matches  709;  Conservative   0;  Mismatches  295;  Indels   6;  Gaps    1;


Qy        80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
             | || || || || || || || || |||||| | || || ||| |||| ||| | |||||||
Db       104 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTGCACCCGAAAGAATATGAGT 163


Qy       140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
             ||||||| |||||| |  || |   ||||||||||||||| || | || ||| ||||
Db       164 GGGTCCTGATCGCCGGGTACATCATCGTGTTCGTCGTGGCTCTCATTGGGAACGTCCTGG 223


Qy       200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
             | ||  |||| ||||||  |||||||||||||||||||| || ||||||||||||| ||||
Db       224 TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA 283


Qy       260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
             | ||  || ||||||||| || || ||||| |  ||||||| ||||| || |||| |||
Db       284 ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCCAGCCACACTGGTCGTGG 343


Qy       320 ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG 379
             | ||||||||| |||||| | || || || || |||| |||||| || || || ||||||||
Db       344 ATATCACTGAGACCTGGTTTTTTGGACAGTCCCTTTGCAAAGTGATTCCTTATCTACAGA 403


Qy       380 CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATG 439
             | |||||| ||||| ||| | || || || || || |||| |||||| |||| || |||||||
Db       404 CCGTGTCGGTGTCTGTGTCTGTCCTCACACTGAGCTGTATCGCCTTGGATCGGTGGTATG 463


Qy       440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG 499
             | |||||| |||||| |  |||| |||||||||||||||| |||||||||| |  ||| |
Db       464 CAATCTGTCACCCTTTGATGTTTAAGAGCACAGCAAAGCGGGCCCGTAACAGCATTGTCA 523


Qy       500 GCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCA 559
             |||||| ||| || ||       || ||| | || |||||       ||||||||| ||||||
Db       524 TCATCTGGATTGTCTCCTGCATTATAATGATTCCTCAGGCCATCGTCATGGAGTGCAGCA 583


Qy       560 GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGG 619
             ||| | || |  |||||||  ||  ||||| | || ||||||||| |||||||
Db       584 CCGTGTTCCCAGGCTTAGCCAATAAAACCACCCTCTTTACGGTGTGTGATGAGCGCTGGG 643


Qy       620 CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCC 679
             | ||| | ||||||||||| |||||||| || |||||| | || || ||| |||| |
Db       644 GTGGTGAAATTTATCCCAAGATGTACCACATCTGTTTCTTTCTGGTGACATACATGGCAC 703


Qy       680 CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA 739
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-Db    704  CACTGTGTCTCATGGTGTTGGCTTATCTGCAAATATTTCGCAAACTCTGGTGTCGACAGA  763.

Qy     740  TCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGG  799
            ||||  ||  ||   |  ||  |  |  |      |  |  ||  |||||||  ||           ||||  |
Db     764  TCCCTGGAACATCATCTGTAGTTCAGAGAAAATGGAAGCCCC------TGCAGCCTGTTT  817

Qy     800  ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAG  859
            |  |    |  ||  |    |        |  ||  |||||    ||||  |   |||||||
Db     818  CACAGCCTCGAGGGCCAGGACAGCCAACGAAGTCCCGGATGAGCGCTGTGGCGGCTGAAA  877

Qy     860  TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCT  919
            |  |||||||||  ||  ||   |  |||||  |||        ||||  |||||||  |||||   |||||  |
Db     878  TAAAGCAGATCCGAGCCAGAAGGAAAACAAAACGGATGTTGATGGTTGTGCTTTTGGTAT  937

Qy     920  TCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGT  979
            |  ||   |  |||||  ||  ||  ||   |||  ||||||||||  ||  |||||  ||  ||  |||||||
Db     938  TTGCAATTTGCTATCTACCAATTAGCATCCTCAATGTGCTAAAGAGAGTATTTGGGATGT  997

Qy     980  TCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGG  1039
            |      |||  |       |||  |  ||    ||||  ||  |||||  ||  |||||  ||  |||||||||  |
Db     998  TTGCCCATACTGAAGACAGAGAGACTGTGTATGCCTGGTTTACCTTTTCACACTGGCTTG  1057

Qy .   1040 TGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGGA  1089
            |  ||  ||||||  ||  |||||  ||  ||  ||  ||  ||  ||  ||  |||||||||||
Db     1058 TATATGCCAATAGTGCTGCGAATCCAATTATTTATAATTTTCTCAGTGGA  1107
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Search completed: October 16, 2004, 03:40:45
Job time : 587.359 secs